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OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 18:07:47 / Search time 8941 Seconds

(without alignments)
11597.602 Million cell updates/sec

Title: US-10-627-886-1

Perfect score: 2140
Sequence: 1 CTCCTTGTGCTGCGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY_NUC

Gapop 10.0 / Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2140	100.0	2140	6	AR086858 Sequence
2	2137	99.9	2137	6	AR086871 Sequence
3	2046	95.6	2099	6	AR086859 Sequence
4	2043	95.5	2096	6	AR086872 Sequence
5	2012.8	94.1	2145	8	CSNADP
6	1969	92.0	1969	6	AR086860 Sequence
7	1501.4	70.2	1506	6	AR086876 Sequence
8	1470	68.7	1473	6	AR086877 Sequence
9	592.2	27.7	10256	1	AE004872 Pseudomonas
10	572.2	26.8	1628	1	PAE15166 Pseudomonas
11	572.4	26.7	11163	1	AE014684 Bifidobac
12	572.4	26.7	349980	6	AX492783 Sequence
13	572.4	26.7	349980	6	AX553950 Sequence
14	565.2	26.4	1628	1	PAE18494 Pseudomonas
15	554.4	25.9	292100	1	SC093121 Streptomy
16	551.6	25.8	110000	1	AP006618_47 Continuation (48 o
17	551.6	25.8	9872	8	CGSDHANC
18	548.6	25.6	1691	3	GIANADPDGH
19	541	25.3	1113	3	AF533883 Spironuc

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22	529.2	24.7	348171	1	BX640412 Bordetell
23	526	24.6	104170	2	AC091510 Leishmani
24	523	24.4	10495	1	AE002013 Deinococc
25	515.8	24.1	346259	1	BX640435 Bordetell
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ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	1	from patent US 5985634.	DNA	linear	PAT 07-SEP-2000
AR086858	AR086858	Sequence 1	2140 bp				
AR086858	AR086858	Accession					
VERSION	AR086858.1	GI:10013624					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	Unclassified.						
AUTHORS	1 (bases 1 to 2140)						
TITLE	Schmidt, R.R. and Miller, P.						
JOURNAL	Polypeptides and polynucleotides relating to the alpha- and						
FEATURES	.beta. subunits of glutamate dehydrogenases and methods of use						
source	Patent: US 5985634-A 1 16-NOV-1999;						
	Location/Qualifiers						
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	/organism="Unknown"						
	/mol_type="unassigned DNA"						
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Best Local Similarity	100.0%; Pred. No. 1.5e-242;						
Matches 2140; Conservative	0; Mismatches 0; Indels 0; Gaps 0;						
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QY	121 TCCGTCGCCAAGGCGCATGTCGCGCGCAAGCGCGTCTCGTGGAGAGAGATCTCG 180						
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QY	181 CGATGACGCCACCAACCGGCACTTACGCGCTGACAGAGCGGTGAAGAGATGCGCA 240						
DB	181 CGATGACGCCACCAACCGGCACTTACGCGCTGACAGAGCGGTGAAGAGATGCGCA 240						
QY	241 CCAAGCGCGGACCTGAGGCGCTGTGTCACGCGGATTCAGAACCCGACCTGCGCACGCTGC 300						

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Gy 361 TGGCGGTCTCCCTGAGCGCCGTGTGTGAGAAAGCGCCGAGGTGTGCGCAATCTTCAAGC 420
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Db 1501 AGAATCCGCGATGAGGCGGTCCCGCAGATGAAATGTTGATGCTGCTGCGGCGCAACA 1560
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RESULT 2
AR086871
LOCUS AR086871 2137 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 18 from patent US 5985634.
ACCESSION AR086871
VERSION AR086871.1 GI:10013637
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2137)
AUTHORS Schmidt,R.R. and Miller,P.
TITLES Polypeptides and polynucleotides relating to the .alpha.- and
beta.-subunits of glutamate dehydrogenases and methods of use
JOURNAL Patent: US 5985634-A 18-16-NOV-1999;
FEATURES
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location/Qualifiers
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DEFINITION	Sequence 3 from patent US 5985634.	linear	PAT 07-SEP-2000
ACCESSION	AR086859		
VERSION	AR086859.1	GI:10013625	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2099)		
TITLE	Schmidt, R. R. and Miller, P.		
JOURNAL	Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use		
FEATURES	Patent: US 5985634-A 3 16-NOV-1999;		
source	Location/Qualifiers		
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Best Local Similarity	98.0%;	Pred. No. 1.7e-231;	
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OY	901	ACGGCGCGTCTGCTTTTGTGGAGAACGTGCTGACAGACCAAGGGCGGAGGCTTCAAGGGCA	960
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Db	1459	ACGACTCCGCGCAATGGGGCGGTCCGCGAGTACAATTTGTAACCTGGTGGGGGCGCAACA	1518
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Db	1519	TCGCGGGCTTCAACAAGGTGAGTGCAGTACAGGCGCCAGGGCGCTGTTTAAGCTGCC	1578
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Db	1579	AGGCCCAAGCAACGCGCTCACCGGCAATTCACCCAACTCAACGSCCAAGACCTTTT	1638
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Db 2059 GTAAACAGACGAGTCAAAAAA 2098

RESULT 4
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LOCUS AR086872 Sequence 19 from patent US 5985634.
ACCESSION AR086872
VERSION AR086872.1 GI:10013638
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2096)
AUTHORS Schmidt,R.R. and Miller,P.
TITLE Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use
JOURNAL Patent: US 5985634-A 19 16-NOV-1999;
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 95.5%; Score 2043; DB 6; Length 2096;
Best Local Similarity 98.0%; Pred. No. 3,8e-231;
Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

Qy 4 CTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
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Db 61 TGGCC-----TGGCGGTGGATTC 78
Qy 124 GCTCGCGCAAGCGCATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGAGATCTCGCGA 183
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 X58832
 ACCESSION X58832.1 GI:18272
 VERSION NADP-gdh gene; NADP-specific glutamate dehydrogenase.
 KEYWORDS Chlorella sorokiniana
 SOURCE Chlorella sorokiniana
 ORGANISM Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae;
 Chlorellales; Chlorellaceae; Chlorella.
 REFERENCE 1
 AUTHORS Cook,J.M., Kim,K.D., Miller,P.W., Hutson,R.G. and Schmidt,R.R.
 TITLE A nuclear gene with many introns encoding ammonium-inducible
 chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella
 sorokiniana
 JOURNAL Plant Mol. Biol. 17 (5), 1023-1044 (1991)
 MEDLINE 92032762

PUBMED 1718478
 REFERENCE 2 (bases 1 to 2145)
 AUTHORS Schmidt,R.R.
 TITLE Direct Submission
 JOURNAL Submitted (03-APR-1991) R.R. Schmidt, University of Florida, Dept
 of Microbiology and Cell Biology, 3103 McCarty Hall, Gainesville FL
 32611, USA
 COMMENT See X58831 for related sequence
 ATTENTION: X58831 and X58832 were incorrectly reported as having
 one accession number (X58832) in the reference [2].
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LOCUS AR086876 1506 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 23 from patent US 598564.
ACCESSION AR086876
VERSION AR086876.1 GI:10013642
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Schmidt, R.R. and Miller, P.

TITLE Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use
JOURNAL Patent: US 5985634-A 23 16-NOV-1999;
FEATURES Location/Qualifiers
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DEFINITION Sequence 25 from patent US 5985634.
ACCESSION AR086877
VERSION AR086877.1 GI:10013643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Schmidt,R.R. and Miller,P.
TITLE Polypeptides and polynucleotides relating to the .alpha.- and .beta.-subunits of glutamate dehydrogenases and methods of use
JOURNAL Patent: US 5985634-A 25 16-NOV-1999;
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 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 1 (bases 1 to 10256)
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S.L., Huftnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.U., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Retter, J., Sater, M.H., Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 TITLE
 JOURNAL NATURE 406 (6799), 959-964 (2000)
 MEDLINE 20437337
 PUBMED 10984043

REFERENCE
 AUTHORS
 2 (bases 1 to 10256)
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S.L., Huftnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.U., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Retter, J., Sater, M.H., Hancock, R.E.W., Lory, S., and Olson, M.V.
 TITLE
 JOURNAL Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
 3 (bases 1 to 10256)

REFERENCE
 AUTHORS
 Pseudomonas aeruginosa Community Annotation Project (PseudocAP)
 TITLE
 JOURNAL Direct Submission
 JOURNAL Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada

COMMENT
 This represents the February 3, 2003 version of the continually updated, reviewed, *Pseudomonas aeruginosa* PA01 genome annotation, from PseudocAP (see <http://www.pseudomonas.com> for latest updates and links to alternate annotations). PseudocAP is coordinated by

Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert B.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.

'Protein name confidence' is used to rate our confidence of the accuracy of the protein name.

Class 1: Function experimentally demonstrated in *P. aeruginosa*.

Class 2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).

Class 3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.

Class 4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.

Location/Qualifiers

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Best Local Similarity 68.1%; Pred. No. 8,4e-61;

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RESULT 10

PAE1516

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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AUTHORS

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 ORGANISM Bifidobacterium longum NCC2705
 Bifidobacterium longum NCC2705
 Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
 REFERENCES
 1 (bases 1 to 11163)
 Schell, M.A., Karmirantzou, M., Snel, B., Vilanova, D., Berger, B., Pessi, G., Zwielen, M.-C., Desiere, F., Bork, P., Delley, M., Pridmore, D. and Arigoni, F.
 The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract
 Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14422-14427 (2002)
 2 (bases 1 to 11163)
 Schell, M.A., Karmirantzou, M., Snel, B., Vilanova, D., Berger, B., Pessi, G., Zwielen, M.-C., Desiere, F., Bork, P., Delley, M., Pridmore, D. and Arigoni, F.
 Direct Submision
 Submitted (27-AUG-2002) Bioscience, Nestle Research Center, P.O. Box 44, Lausanne 26 1000, Switzerland
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TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS

FEATURES
 source

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Best Local Similarity 66.9%; Pred. No. 1.7e-58;

Matches 886; Conservative 0; Mismatches 411; Indels 27; Gaps 4;

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QY 839 GGTGTGACCCCGAAGGCGCAGAGTATGGCGCTCCAGATCCGCGCGGAGCCACCGG 898
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QY 899 CTAGGCGCCGCTGCTGTTTGTGAGAACGTGTGTAAGAACAGG---CGAGGCTTCA 955
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RESULT 12

AX492783 349980 bp DNA linear PAT 26-SEP-2002

LOCUS AX492783 Sequence 1101 from Patent EP1227152.

ACCESSION AX492783

VERSION AX492783.1 GI:23338466

KEYWORDS

SOURCE Bifidobacterium longum biovar Longum

ORGANISM Bifidobacterium longum biovar Longum

REFERENCE 1 Bacterial strain and genome of Bifidobacterium

AUTHORS Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;

JOURNAL Bifidobacteriaceae; Bifidobacterium.

FEATURES

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/mol_type="unassigned DNA"

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/note="1106 seq in place of 1099 because seq 1 (2.256.638

bases splitied-in 7 more sequences.-seq 0001: from

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0.300.001 to 0.649.980 length: 349980-seq 1101: from

0.600.001 to 0.949.980 length: 349980-seq 1102: from

0.900.001 to 1.249.980 length: 349980-seq 1103: from

1.200.001 to 1.549.980 length: 349980-seq 1104: from

1.500.001 to 1.849.980 length: 349980-seq 1105: from

1.800.001 to 2.149.980 length: 349980-seq 1106: from

2.100.001 to 2.256.638 length: 156638"

ORIGIN

Query Match 26.7%; Score 572.4; DB 6; Length 349980;
 Best Local Similarity 66.9%; Pred. No. 8.1e-59;
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Qy      956 GGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
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Qy      1076 CAAGCGCTTCAACCGCGCGAGCTGCAAGCGGTGCAAGCAATCAAGAAAGT-----CGAGCG 182969
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Qy      1550 GGGCGCCCAACATCGCGGCGCTTTCACCAAGTGTGATGCGCGTCAAGGCGCGCGCTGT 1609
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RESULT 13
AX553950 349980 bp DNA linear PAT 27-NOV-2002
LOCUS AX553950
DEFINITION Sequence 4 from Patent WO02074798.
ACCESSION AX553950
VERSION AX553950.1 GI:25897903
KEYWORDS
SOURCE
ORANISM Bifidobacterium longum biovar Longum
Bifidobacterium longum biovar Longum
Bacteria; Actinobacteria; Actinobacteriales;
Bifidobacteriaceae; Bifidobacterium.
REFERENCE
1 Arigoni, F., Delley, M., Mollet, B., Fridmore, R.D., Schell, M.A.,
Pohl, T.G. and Zwielen, M.C.
The genome of a bifidobacterium
Patent: WO 02074798-A 4 26-SEP-2002;
SOCIETE DES PRODUITS NESTLE S.A. (CH)
FEATURES
Location/Qualifiers
source 1..349980
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/note="seq 1: original length 2256646 split into-seq 1:
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0.649.980-seq 4: from 0.600.001 to 0.949.980-seq 5: from
0.900.001 to 1.249.980-seq 6: from 1.200.001 to
1.549.980-seq 7: from 1.500.001 to 1.849.980-seq 8: from
1.800.001 to 2.149.980-seq 9: from 2.100.001 to 2.256.646"

ORIGIN
Query Match 26.7%; Score 572.4; DB 6; Length 349980;
Best Local Similarity 66.9%; Pred. No. 8,1e-59;
Matches 886; Conservative 0; Mismatches 411; Indels 27; Gaps 4;
Qy 305 CGAGATTTTCAATGAAGACCCGAGCAGCAGAGTTCATGCGAGCGGTGCGCGAGTGGC 364
Db 182145 CGAAGTGTGTCGCGTGAAGCGGATCAAGCGGAGTCTCTCAAGCCGTTGCGCGAGTCTT 182204
Qy 365 CGTCTCCCTGAGCGCGTGTTCGAGAGCGCC-----GAGTGTGCTGCCATCTTCAA 418
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OY	1376	CGGCAAG	CGGCGCA	CGCGCGG	CGGTG	CAGCGG	CTGAGATG	ATACCCAGAACG	1435			
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OY	1436	CATG	AGCCTG	AACTG	GAATCTG	CGGAC	CAAGCTG	AGCGCATG	AAAGA	1495		
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OY	1496	CATCA	AGACT	CCGCA	TAGGGGCG	GTCC-----	CGCAAT	CAATGTTG	ACTGTG	1549		
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OY	1550	GGGCG	CCCA	CATCG	CGGCTT	CA	CAAGGTG	GTGCTG	CTCAAG	CGCCAGGCGCTGT	1609	
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DEFINITION	Pseudomonas aeruginosa gdhA gene, strain PAC1.				
VERSION	Y18494				
KEYWORDS	Y18494.1 GI:4239790				
SOURCE	gdhA gene; NADP-glutamate dehydrogenase.				
ORGANISM	Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.				
REFERENCE	1				
AUTHORS	Ansari, F.				
JOURNAL	Thesis (1994) University of London London U.K				
REFERENCE	2 (bases 1 to 1628)				
AUTHORS	Brown, P.R.				
TITLE	Direct Submision				
JOURNAL	Submitted (21-OCT-1997) P.R. Brown, Kings College London, Molecular Biology and Biophysics Group, Strand, London, WC2R 2LS, UK				
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ORIGIN					
Query Match	26.4%; Score 565.2; DB 1; Length 1628;				
Best Local Similarity	66.9%; Pred. No. 1.9e-57;				
Matches 871; Conservative	0; Mismatches 413; Indels 18; Gaps 4;				
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381	GTGTTCAAGAACGCCGCCGAGCTGCTG-----CCCATCTTCAACAGATCGTTGAGCT	434			
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Db 1056 GTGATGT 1115
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Db 1116 CAGT 1172
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Db 1230 ---GATATCGGCGT 1286
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Db 1287 CTGT 1346
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Qy 1395 GCGCGCGT 1454
Db 1407 GCGCGCGT 1466
Qy 1455 GCGCGAGAGT 1514
Db 1467 GAGGCGGAGT 1526
Qy 1515 GGGCGGT 1571
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Qy 1572 ACCAAGT 1613
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RESULT 15
SC0939121

LOCUS SC0939121 292100 bp DNA linear BCT 11-FEB-2003
DEFINITION Streptomyces coelicolor A3(2) complete genome; segment 18/29.
ACCESSION AL939121 AL031317 AL161691 AL161755 AL161803 AL353872
VERSION AL356832 AL389898 AL450450 AL451182 AL589164 AL645882
KEYWORDS AL939121.1 GI:24429533
SOURCE Streptomyces coelicolor A3(2)
ORGANISM Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycetaceae; Streptomyces.
REFERENCE 1 Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L., Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H., Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M., Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S., Huang, C.H., Kieiser, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S., Rabinowitz, E., Rajandream, M.A., Rutherford, K., Rutter, S., Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S., Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrrell, B.G., Parkhill, J. and Hopwood, D.A.
TITLE Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)
JOURNAL Nature 417 (6885), 141-147 (2002)
MEDLINE 21996410
PUBMED 12000953
REFERENCE 2 (bases 1 to 292100)
Bentley, S.D.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces Sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sds@sanger.ac.uk
COMMENT On or before Oct 30, 2002 this sequence version replaced gi:3449234, gi:7288050, gi:7320887, gi:7321265, gi:7649562, gi:8218190, gi:9367445, gi:11544744, gi:20520684.
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Job time : 8951 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 17:34:32 ; Search time 1075 Seconds
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Title: US-10-627-886-1

Perfect score: 2140

Sequence: 1 CTCCTTCTGCTGCGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 13: geneseqn2004cs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2140	100.0	2140	2	AAT64529
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5	2046	95.6	2099	2	AAT64530
6	2046	95.6	2099	6	ABK51008
7	2043	95.5	2096	6	AAT64543
8	2043	95.5	2096	6	ABK51021
9	2040	95.3	2124	12	ADQ36706
10	1969	92.0	1969	2	AAT64531
11	1969	92.0	1969	6	ABK51009
12	1935.8	90.5	2083	12	ADQ36708
13	1691	79.0	2084	12	ADQ36723
14	1611	75.3	2045	12	ADQ36724
15	1565	73.1	1922	12	ADQ36712
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26	529.2	24.7	1392	8	ACA27224	ACA27224 Prokaryot
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29	500.4	23.4	1314	13	AD558634	Ad558634 Bacterial
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34	472.6	22.1	1332	8	AA597271	AA597271 Neisseria
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36	469.2	21.9	1242	10	AB238921	Ab238921 N. gonorr
37	467.6	21.9	35133	3	AAA81518	AAA81518 N. mening
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42	447	20.9	1341	8	ACA36189	ACA36189 Prokaryot
43	436	20.4	1344	5	AAf87488	AAf87488 Brevibact
44	435.8	20.4	349980	5	AAH68531	AAH68531 C. glutami
45	435.6	20.4	2190	2	AAQ37237	AAq37237 gdhA gene

ALIGNMENTS

RESULT 1	
ID	AAT64529 standard; CDNA; 2140 BP.
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XX	AAT64529;
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DT	17-OCT-2003 (revised)
DT	10-JUL-1997 (first entry)
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DE	NADP-specific glutamate dehydrogenase alpha-subunit precursor CDNA.
XX	
XX	Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW	chloroplast; transgenic plant; ds.
XX	
OS	Chlorella sorokiniana; strain UTEX 1230.
XX	
XX	
FT	Key
FT	location/Qualifiers
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FT	CDs
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XX	(UYFL) UNIV FLORIDA.
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PI	Schmidt RR, Miller P;
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DR	WPI: 1997-226226/20.
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XX	P-PSDB; AAM15407.
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PT	DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT	sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT	plant cells.
XX	

DB 1801 CGGCTATTTTTCGCGACGCGCGCTCAACCCGAGAGCCTCTCTCCCGGAGCCCTTAAGC 1860
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RESULT 2
ABKS1007
ID ABKS1007 standard; cDNA; 2140 BP.
XX
AC ABKS1007;
XX
DT 24-SEP-2002 (first entry)
XX
XX cDNA encoding NADP-glutamate dehydrogenase alpha subunit.
XX
XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
XX ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.
XX
OS Chlorella sorokiniana.
XX
FH Key Location/Qualifiers
FT CDS 33..1613
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FT /product= "NADP-specific glutamate dehydrogenase alpha
FT subunit"
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XX PD 23-MAY-2002.
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XX PE 01-MAY-1998; 98US-00070844.
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XX PR 01-MAY-1998; 98US-00070844.
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XX PA (SCHMIDT R R.
XX (MILLER) MILLER P.
XX
XX PI Schmidt RR, Miller P;
XX
XX WI; 2002-499691/53.
XX P-PSDB; AAU98950.
XX
XX PT Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
XX tolerance.
XX
XX PS Disclosure; Page 11-13; 35pp; English.
XX
XX The invention relates to a method of modulating nitrogen metabolism in
XX plant cells, comprising transforming a plant cell with a polynucleotide
XX encoding a polypeptide having glutamate dehydrogenase activity, and
XX culturing the cell to produce descendant cells which express the
XX polypeptide. The method is used to provide plants with increased yield.

CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the coding sequence of Chlorella sorokiniana
CC NADP-glutamate dehydrogenase alpha subunit, used in the method of the
XX invention
SQ Sequence 2140 BP; 416 A; 734 C; 632 G; 358 T; 0 U; 0 Other;
Query Match 100.0%; Score 2140; DB 6; Length 2140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CTCCTTTTGTCTGCGCCCTCTCTCGTCCGCGCATGACAGCCGCTCTGCGCAAGCTTA 60
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DB 481 ACCTGCAAGTCAACCGCGGCTTCCGCTGCGAGTACTGTCGCGCATTCGCGCATCAAGG 540
QY 541 GCGGCTGCGGCTTCAACCCCTCCGAGAACCTGTCATCATGAGTTCTTGGCTTGAAGC 600
DB 541 GCGGCTGCGGCTTCAACCCCTCCGAGAACCTGTCATCATGAGTTCTTGGCTTGAAGC 600
QY 601 AGATCTTCAAGAGAGCTGAGCAACCCCTGAGAGCGCGGAGAGGCGGCTTCCGACT 660
DB 601 AGATCTTCAAGAGAGCTGAGCAACCCCTGAGAGCGCGGAGAGGCGGCTTCCGACT 660
QY 661 TCGACCCCAAGGCGAAGAGCGAGCGAGTGTGCTTCTGCGCATGCTTCAATGAGCG 720
DB 661 TCGACCCCAAGGCGAAGAGCGAGCGAGTGTGCTTCTGCGCATGCTTCAATGAGCG 720
QY 721 AGCTGACGCGGCATCATGAGTACGAGAGCGAGCGCGCGGAGAGTCTGCGCGGAGCG 780
DB 721 AGCTGACGCGGCATCATGAGTACGAGAGCGAGCGCGCGGAGAGTCTGCGCGGAGCG 780
QY 781 CCGCGAGATTTGGCTACTTTTTCGCGCAGTACCAAGCGCATCAAGAGACTTCAACCGCG 840
DB 781 CCGCGAGATTTGGCTACTTTTTCGCGCAGTACCAAGCGCATCAAGAGACTTCAACCGCG 840
QY 841 TGTGACCCCGCAAGGCGCGAGATGAGCGCGCTCGAGATTCGCGCGAGCGCGAGCT 900
DB 841 TGTGACCCCGCAAGGCGCGAGATGAGCGCGCTCGAGATTCGCGCGAGCGCGAGCT 900
QY 901 ACGGCGCGTGTCTGTTGTGAGAGAGTGTGAAGAGCAAGAGCGAGAGCTCAAGGAGCA 960

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Db      |||
901  ACGGCGCGTGCTGTTTGTGGAGAACTGCTGAAGACAAAGGCGAGCGCTCAAGGGCA 960
Qy      |||
961  AGCGTGCTGCTGTCTCTGCGCGCGGCAACGTGCGCCAGTATCTGCGCGAGCTGCTGCTG 1020
Db      |||
961  AGCGTGCTGCTGTCTGCGCGCGGCAACGTGCGCCAGTATCTGCGCGAGCTGCTGCTG 1020
Qy      |||
1021  AGAAGGCGCGCATGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db      |||
1021  AGAAGGCGCGCATGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy      |||
1081  GCTTCACGCGCGAGAGCTGCAAGGCGGTGCAAGACATGAAGAAAGAAACAACAGCGGCC 1140
Db      |||
1081  GCTTCACGCGCGAGAGCTGCAAGGCGGTGCAAGACATGAAGAAAGAAACAACAGCGGCC 1140
Qy      |||
1141  GCATCTCCGAGTACAAAGACCAACCGCGCTGTATGTGGGGGACCGCGCGCAAGCTTTGG 1200
Db      |||
1141  GCATCTCCGAGTACAAAGACCAACCGCGCTGTATGTGGGGGACCGCGCGCAAGCTTTGG 1200
Qy      |||
1201  AGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGCGCGCAACCGAAGATCGATGAGC 1260
Db      |||
1201  AGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGCGCGCAACCGAAGATCGATGAGC 1260
Qy      |||
1261  ACGACGCGGAGCTGCTGATCAAGCAAGCGCTGCAGTACGTGGTGGAGGCGCGCAATGC 1320
Db      |||
1261  ACGACGCGGAGCTGCTGATCAAGCAAGCGCTGCAGTACGTGGTGGAGGCGCGCAATGC 1320
Qy      |||
1321  CCTCCACCAAGAGGCTTCCACAAAGTACAAAGAGCGGCGCATCTACTACTGCGCGGCA 1380
Db      |||
1321  CCTCCACCAAGAGGCTTCCACAAAGTACAAAGAGCGGCGCATCTACTACTGCGCGGCA 1380
Qy      |||
1381  AGGCGGCGCAAGCGCGCGCGCGGTGAGCGGCTGAGGCGCTGAGATGACCCAGAACCGCATGA 1440
Db      |||
1381  AGGCGGCGCAAGCGCGCGCGCGGTGAGCGGCTGAGGCGCTGAGATGACCCAGAACCGCATGA 1440
Qy      |||
1441  GCCTGAAGTGAAGCTGCGAGAGAGTTCGCGACAAAGCTGAGAGCGCATCAATGAAGACATCT 1500
Db      |||
1441  GCCTGAAGTGAAGCTGCGAGAGAGTTCGCGACAAAGCTGAGAGCGCATCAATGAAGACATCT 1500
Qy      |||
1501  ACGACTCCGCGCATGAGGCGCGTCCCGCAATACAAAGTGAAGCTGCTGCGCGCGCAACA 1560
Db      |||
1501  ACGACTCCGCGCATGAGGCGCGTCCCGCAATACAAAGTGAAGCTGCTGCGCGCGCAACA 1560
Qy      |||
1561  TCGCGGCGCTTCCAAAGGTGCTGATGCGCTCAAGGCGCGCAAGGCGCTGTTAAGTGGCC 1620
Db      |||
1561  TCGCGGCGCTTCCAAAGGTGCTGATGCGCTCAAGGCGCGCAAGGCGCTGTTAAGTGGCC 1620
Qy      |||
1621  AGGCGCAAGCGAGCTGCAAGGCGCATCAAGCGCAAGCGCAAGCGCGCAAGCGCTTTT 1680
Db      |||
1621  AGGCGCAAGCGAGCTGCAAGGCGCATCAAGCGCAAGCGCAAGCGCGCAAGCGCTTTT 1680
Qy      |||
1681  CGGAAAGCGGCGCTTTTCCGAGCGGCGCTCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db      |||
1681  CGGAAAGCGGCGCTTTTCCGAGCGGCGCTCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCT 1740
Qy      |||
1741  GCGCGCGTGGCGCGCAATTCACCGCAAGAAAGTACGCGCGCATCTGATGCTGATCAGAGA 1800
Db      |||
1741  GCGCGCGTGGCGCGCAATTCACCGCAAGAAAGTACGCGCGCATCTGATGCTGATCAGAGA 1800
Qy      |||
1801  CGGCTATTTTTCGCGAGCGCGCTCAAGCGCGAGCTGCTGCTGCGCGCGCGCTTAAAGC 1860
Db      |||
1801  CGGCTATTTTTCGCGAGCGCGCTCAAGCGCGAGCTGCTGCTGCGCGCGCGCTTAAAGC 1860
Qy      |||
1861  GCTGACGTCGCGCGCACTTGTGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db      |||
1861  GCTGACGTCGCGCGCACTTGTGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy      |||
1921  CACCGTGTGTGAAGCTACAGCTCAATGCTTTTGTGATGTGGCGCGCGCTGCTGCTGCTG 1980
Db      |||
1921  CACCGTGTGTGAAGCTACAGCTCAATGCTTTTGTGATGTGGCGCGCGCTGCTGCTGCTGCTG 1980
Qy      |||
1981  CCGCGAATTTTCTCTGCAATGAGACGTGCGGTTCCTAGCTGTGTCACCGCAAGTACAGTT 2040
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Db      |||
1981  CCGCGAATTTTCTCTGCAATGAGACGTGCGGTTCCTAGCTGTGTCACCGCAAGTACAGTT 2040
Qy      |||
2041  AGTGTGGTGCTGCTGCGCTGCGCGCGGATGCGATGCTGATGCTGAGAGTGTGT 2100
Db      |||
2041  AGTGTGGTGCTGCTGCGCTGCGCGCGGATGCGATGCTGATGCTGAGAGTGTGT 2100
Qy      |||
2101  GTAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db      |||
2101  GTAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140

RESULT 3
AAT64542
ID AAT64542 standard; cDNA; 2137 BP.
XX
AC AAT64542;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE NADP-specific glutamate dehydrogenase alpha-subunit precursor cDNA.
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant; ds.
OS Chlorella sorokiniana; strain UTEX 1230.
XX
FH Key Location/Qualifiers
FT CDS 30..1610
FT /*tag= a
FT translat_peptide 30..149
FT /*tag= b
FT mat_peptide 150..1607
FT /*tag= c

XX
PN M09712983-A1.
XX
PD 10-APR-1997.
XX
PE 03-OCT-1996; 96WO-US015921.
XX
PR 06-OCT-1995; 95US-00541033.
XX
PA (UYFL ) UNIV FLORIDA.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 1997-226226/20.
XX
DR P-PSDB; AAM15407.
XX
PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
XX
PS Claim 2; Page 40-41; 61p; English.
XX
CC cDNA clones (AAT64542 and AAT64543) respectively code for the alpha
CC subunit (AAM15407) and beta subunit (AAM15408) precursor proteins of an
CC ammonium-inducible, chloroplast-localised NADP-specific glutamate
CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obt. by
CC ligation of 3' clone pBGD53 (AAT64531) and 5' clones pBG63 (AAT64540)
CC and pBG64 (AAT64541). The proteins are processed to yield mature alpha
CC and beta subunits (see also AAT64547-48) that comprise the active NADP-
CC GDH hexameric isoenzymes. The nitrogen metabolism of plants can be
CC modulated (pref. by increasing assimilation of inorganic N into organic
CC N) by transforming them with nucleotide sequences encoding the alpha
CC and/or beta subunits. Such plants show improved properties, e.g.
CC increased crop yield and improved stress tolerance. Heterohexamers having
CC alpha and beta subunits can be expressed that have higher
CC aminating/deaminating activity ratios (i.e. higher capacity for glutamate
CC synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS
CC field)
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Sequence 2137 BP, 416 A, 732 C, 632 G, 357 T, 0 U, 0 Other;
Query Match 99.9%; Score 2137; DB 2; Length 2137;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 CTTTGTGCTGCGCTCTCTCTCCGTCGCGCATGACAGCCGCTCGTCCGCAAGCCATG 63
1 CTTTGTGCTGCGCTCTCTCTCCGTCGCGCATGACAGCCGCTCGTCCGCAAGCCATG 60
64 TGGCCGCCCGCTGCGCGGACGCGCGCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 123
61 TGGCCGCCCGCTGCGCGGACGCGCGCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 120
124 GCTCCGCCAAGGCGCATGTCGCGCGCAAGCGCGCTGCGCTGCGCGCATGTCGCGCA 183
121 GTCGCGCAAGGCGCATGTCGCGCGCAAGCGCGCTGCGCTGCGCGCATGTCGCGCA 180
184 TGGACGCCACACCGCGCATTCACGCGCGCTGCGCGCATGAGAGCGATGCGACCA 243
181 TGGACGCCACACCGCGCATTCACGCGCGCTGCGCGCATGAGAGCGATGCGACCA 240
244 AGCGCGGACCTGAGGCGCTGCGCGCATGAGAGCGCGCATGCGCGCATGCGCGCA 303
241 AGCGCGGACCTGAGGCGCTGCGCGCATGAGAGCGCGCATGCGCGCATGCGCGCA 300
304 CGGAAATCTTCAAGAGGACCGCGCGCATGAGAGCGCGCATGAGAGCGCGCATGAG 363
301 CGGAAATCTTCAAGAGGACCGCGCGCATGAGAGCGCGCATGAGAGCGCGCATGAG 360
364 CGGTCTCCCTGCGCGCGCTGCGCGCATGAGAGCGCGCATGCGCGCATGCGCGCA 423
361 CGGTCTCCCTGCGCGCGCTGCGCGCATGAGAGCGCGCATGCGCGCATGCGCGCA 420
424 TCGTTGAGCTGAGCGCGCTGATCACCTTCGCGGTCTGCGCTGAGACGCGCGCAAC 483
421 TCGTTGAGCTGAGCGCGCTGATCACCTTCGCGGTCTGCGCTGAGACGCGCGCAAC 480
484 TGGAGGTCAACCGCGCGCTTCGCGGTGAGTACTGTCGCGCATGCGCGCATGAGAGG 543
481 TGGAGGTCAACCGCGCGCTTCGCGGTGAGTACTGTCGCGCATGCGCGCATGAGAGG 540
544 GCTGCGCTTCCACCGCTCGGGAACCTGTCATGAGAGTTCGTCGCTTGAAGCA 603
541 GCTGCGCTTCCACCGCTCGGGAACCTGTCATGAGAGTTCGTCGCTTGAAGCA 600
604 TCTTCAAGAACGCTGACACACCTGCGCATGAGAGGCGCGCTTCGCACTTCG 663
601 TCTTCAAGAACGCTGACACACCTGCGCATGAGAGGCGCGCTTCGCACTTCG 660
664 ACCCAAGGCGCAAGCGGACGCGGAGTATGCGCTTTCGCGCATGAGAGGCGG 723
661 ACCCAAGGCGCAAGCGGACGCGGAGTATGCGCTTTCGCGCATGAGAGGCGG 720
724 TGCAGCGGCACATGAGTACGTCAGAGGAGCGTCCGCGCGGACATGCGCGCGGCGG 783
721 TGCAGCGGCACATGAGTACGTCAGAGGAGCGTCCGCGCGGACATGCGCGCGGCGG 780
784 GCGAGATTGCGTACCTTTTCGCGCGCATGACAGCGCATGACCAAGACTTACACCGCG 843
781 GCGAGATTGCGTACCTTTTCGCGCGCATGACAGCGCATGACCAAGACTTACACCGCG 840
844 TGCACCCGAGGCGCAAGAGTATGCGCGCTCCGAGATCCGCGCGGACACCGGCTACG 903
841 TGCACCCGAGGCGCAAGAGTATGCGCGCTCCGAGATCCGCGCGGACACCGGCTACG 900
904 GCGCGGTGCTGTTTGAAGACGTCGAGAGGACCAAGGCGGAGCTTCAAGGCGCAAGC 963
901 GCGCGGTGCTGTTTGAAGACGTCGAGAGGACCAAGGCGGAGCTTCAAGGCGCAAGC 960
964 GCTGCTGTGTCTGCGCGGCAAGTATGCGCGCATGAGAGGCGGAGCTGCTGAGAG 1023
961 GCTGCTGTGTCTGCGCGGCAAGTATGCGCGCATGAGAGGCGGAGCTGCTGAGAG 1020

1024 AGGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
1021 AGGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1084 TCACGCGGAGGAGCTGAGGCGGCTGAGGAGCATGAGAGAGAGAGAGAGAGAGAGAG 1143
1081 TCACGCGGAGGAGCTGAGGCGGCTGAGGAGCATGAGAGAGAGAGAGAGAGAGAGAG 1140
1144 TCTCCGAGTACAGAGGAGCAACCGCGCTGATGATGAGGAGAGAGAGAGAGAGAGAG 1203
1141 TCTCCGAGTACAGAGGAGCAACCGCGCTGATGATGAGGAGAGAGAGAGAGAGAGAG 1200
1204 TGGAGTGCAGGTGAGCAATGCGCTTCCGCGCGGACCGCAAGAGAGATGAGAGAG 1263
1201 TGGAGTGCAGGTGAGCAATGCGCTTCCGCGCGGACCGCAAGAGAGATGAGAGAG 1260
1264 AGCGGAGCTGCTGATCAAGGACGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
1261 AGCGGAGCTGCTGATCAAGGACGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
1324 CCACCAAGGAGGCGATCCAGAGTACAAAGGCGGCGATCATCTGCTCCGCGCAAG 1383
1321 CCACCAAGGAGGCGATCCAGAGTACAAAGGCGGCGATCATCTGCTCCGCGCAAG 1380
1384 CGGCGCAAGCGCGCGCGCTGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
1381 CGGCGCAAGCGCGCGCGCTGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
1444 TGAATGGAATCGAGAGAGGTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1503
1441 TGAATGGAATCGAGAGAGGTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1504 ACTCGCGCATGAGGCGCGCTCCGCGAGATCAATGTTGACCTGCGCGCGCGCAATG 1563
1501 ACTCGCGCATGAGGCGCGCTCCGCGAGATCAATGTTGACCTGCGCGCGCGCAATG 1560
1564 CGGCGTTACCAAGTGTGCTGATGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623
1561 CGGCGTTACCAAGTGTGCTGATGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1624 CCAGAGGAGGCTACAGCGGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1683
1621 CCAGAGGAGGCTACAGCGGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
1684 AAGCGCGCTTTTTCGCGAGGAGGCGCTGACCTGCTTCAATACCTGCTATTCG 1743
1681 AAGCGCGCTTTTTCGCGAGGAGGCGCTGACCTGCTTCAATACCTGCTATTCG 1740
1744 GCGGTGCGCTGCAATTCACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1803
1741 GCGGTGCGCTGCAATTCACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
1804 CTATTTTTTTCGAGAGGCGGCTACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1863
1801 CTATTTTTTTCGAGAGGCGGCTACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
1864 GAGGTGCGCGGAGCTTTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1923
1861 GAGGTGCGCGGAGCTTTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
1924 CCTGTTGTAAGGCTTACAGGCTCAATTCCTTTTATGATGATGAGCGCGCTCTGCGCC 1983
1921 CCTGTTGTAAGGCTTACAGGCTCAATTCCTTTTATGATGATGAGCGCGCTCTGCGCC 1980
1984 GGAATTTTTCGAGATGAG 2043
1981 GGAATTTTTCGAGATGAG 2040
2044 GTGCGTGTGCTGCGCGCTGCGCGGAGATGAGATGAGAGAGAGAGAGAGAGAGAG 2103
2041 GTGCGTGTGCTGCGCGCTGCGCGGAGATGAGATGAGAGAGAGAGAGAGAGAGAG 2100


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Db      1261  ACGCCGAGCTGCTGATCAAGCAGCGCTGCAAGTGTGTGAGGGCCCAACATGCTCT 1320
Qy      1324  CCACCAAGAGAGCCATCCACAAGTACACAAAGCCGGCATCATCTACTGCCCCGGCAAG 1383
Db      1321  CCACCAAGAGAGCCATCCACAAGTACACAAAGCCGGCATCATCTACTGCCCCGGCAAG 1380
Qy      1384  CGGCGCAAGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAG 1443
Db      1381  CGGCGCAAGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAG 1440
Qy      1444  TGAACCTGAGCTCGGAGAGAGTTCGCGAACAGCTGAGCGCATCATGAAGACATCTAC 1503
Db      1441  TGAACCTGAGCTCGGAGAGAGTTCGCGAACAGCTGAGCGCATCATGAAGACATCTAC 1500
Qy      1504  ACTCCGCGATGGGGCGGTCCGCGAGATGACATGTTGACTGCTGGCGGGCGCAACATCG 1563
Db      1501  ACTCCGCGATGGGGCGGTCCGCGAGATGACATGTTGACTGCTGGCGGGCGCAACATCG 1560
Qy      1564  CGGGCTTACCAAGGTGCTGATGCGGTCAAGGGCCGAGGGGCTGTTAAGCTGCGCAG 1623
Db      1561  CGGGCTTACCAAGGTGCTGATGCGGTCAAGGGCCGAGGGGCTGTTAAGCTGCGCAG 1620
Qy      1624  CCCAAGCAGCGGCTCACCGGCAATCCAAACCAACTCAACGGCCAGAGACTTTTCGG 1683
Db      1621  CCCAAGCAGCGGCTCACCGGCAATCCAAACCAACTCAACGGCCAGAGACTTTTCGG 1680
Qy      1684  AAGCGGCGCTTTTCCAGCGAGGCGCTCACTGCTGCTTTCATACCTGCTATTGCTC 1743
Db      1681  AAGCGGCGCTTTTCCAGCGAGGCGCTCACTGCTGCTTTCATACCTGCTATTGCTC 1740
Qy      1744  GCGGCGCCCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAACATGACAGAGCG 1803
Db      1741  GCGGCGCCCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAACATGACAGAGCG 1800
Qy      1804  CTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCCCGCGAGCCCTTAAGCGCT 1863
Db      1801  CTATTTTTCGCGACGCGGCTCAACCCGAGAGCTCTCCCGCGAGCCCTTAAGCGCT 1860
Qy      1864  GAGCTCGCGGCTGCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1923
Db      1861  GAGCTCGCGGCTGCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy      1924  CCTTTTGGAGCCCTACAGCTCAATTGCTTTAGTGTAGTGTGTGTGTGTGTGTGTGT 1983
Db      1921  CCTTTTGGAGCCCTACAGCTCAATTGCTTTAGTGTAGTGTGTGTGTGTGTGTGTGT 1980
Qy      1984  CGAATTTTCTGCGATGAGAGTGTGCGGTTCCTAGCGCTGTGACCCCAAGTGAAGT 2043
Db      1981  CGAATTTTCTGCGATGAGAGTGTGCGGTTCCTAGCGCTGTGACCCCAAGTGAAGT 2040
Qy      2044  GTGCGTGTGCTTGCCTGCGCTGCGCGCGAGTGCATGTGTGACCTGAGAGTGTGTGT 2103
Db      2041  GTGCGTGTGCTTGCCTGCGCTGCGCGCGAGTGCATGTGTGACCTGAGAGTGTGTGT 2100
Qy      2104  AACGCGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db      2101  AACGCGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2137

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RESULT 5

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AAAT64530
ID      AAAT64530 standard; cDNA; 2099 BP.
AC      AAAT64530;
XX      17-OCT-2003 (revised)
DT      10-JUL-1997 (first entry)
XX      NADP-specific glutamate dehydrogenase beta-subunit precursor cDNA.
DE      Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KM      chloroplast; transgenic plant; ds.

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XX      Chlorella sorokiniana; strain UTEX 1230.
OS
XX      Key
XX      CDS
XX      Location/Qualifiers
XX      33..1571
XX      /tag= a
XX      translat_peptide 33..140
XX      /tag= b
XX      mat_peptide 141..1568
XX      /tag= c
XX      W09712983-A1.
XX      10-APR-1997.
XX      03-OCT-1996; 96WO-US015921.
XX      06-OCT-1995; 95US-00541033.
XX      (UFL) UNIV FLORIDA.
XX      Schmidt RR, Miller P;
XX      WPI; 1997-226226/20.
XX      P-PSDB; AAM15408.
XX      DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
XX      sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
XX      plant cells.
XX      Claim 2; Page 29-32; 61pp; English.
XX      cDNA clones (AAAT64529 and AAAT64530) respectively code for the alpha
XX      subunit (AAM15407) and beta subunit (AAM15408) precursor proteins of an
XX      ammonium-inducible, chloroplast-localised NADP-specific glutamate
XX      dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were deposited in
XX      E. coli DH5alpha as ATCC 69925 and 69926, respectively. The precursor
XX      proteins are processed to mature alpha and beta subunits (see also
XX      AAAT64547-48) that comprise active NADP-GDH hexameric isoenzymes. The
XX      nitrogen metabolism of plants can be modulated (pref. increasing the
XX      assimilation of inorganic nitrogen into organic nitrogen) by transforming
XX      them with nucleotide sequences encoding the alpha and/or beta subunits.
XX      Such plants show improved properties, e.g. increased crop yield and
XX      improved stress tolerance. Heterohexamers having alpha and beta subunits
XX      can be expressed that have higher amulating/deamulating activity ratios
XX      (i.e. higher capacity for glutamate synthesis) than homohexamers.
XX      (Updated on 17-OCT-2003 to standardise OS field)
SQ      Sequence 2099 BP; 416 A; 713 C; 616 G; 354 T; 0 U; 0 Other;
Query Match 95.6%; Score 2046; DB 2; Length 2099;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
Qy      1 CTCCTTTCTGCGCCCTCTCTCGTCCCGCAAGCAGACCGCCCTGTGCCCAAGCTTA 60
Db      1 CTCCTTTCTGCGCCCTCTCTCTCGTCCCGCAAGCAGACCGCCCTGTGCCCAAGCTTA 60
Qy      61 TCGTGCGCGCCCGCTGCGGCAAGCGCGCGCTGCTGCGCGCGTGGCCGTGCGCGTGG 120
Db      61 TCGTGCGCC-----TGGCGTGG 78
Qy      121 TCGGCTCCGCAAGCGGATGTCGCGCCCAAGCGCGTGTGCTGAGAGAGCATCTTCG 180
Db      79 TCGGCTCCGCAAGCGGATGTCGCGCCCAAGCGCGTGTGCTGAGAGAGCATCTTCG 138
Qy      181 CGATGACGCGACCAACCGGCACTTCAAGCGCGTGCAGAAAGCGGTAAAGATGTGCCA 240
Db      139 CGATGACGCGACCAACCGGCACTTCAAGCGCGTGCAGAAAGCGGTAAAGATGTGCCA 198
Qy      241 CCAAGCGGCGCATGAGGCGCTGTGTCAGCGCATCAAGAACCCCGAGTGGCGCAGCTGC 300
Db      199 CCAAGCGGCGCATGAGGCGCTGTGTCAGCGCATCAAGAACCCCGAGTGGCGCAGCTGC 258

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QY	301	TCACCGAGATCTTCAATGAAGACCCCGAGCAACGAGAGTTATGACGCGGTGCGCAAG	360
Db	259	TGACCCGAGATCTTCAATGAAGACCCCGAGCGACGAGAGTTATGACGCGGTGCGCAAG	318
QY	361	TGGCGGTCTCCCTGACGCGGTGTTCCAGAAAGCGCCCGACCTGTGCGCATCTTCAAGC	420
Db	319	TGGCGGTCTCCCTGACGCGGTGTTCCAGAAAGCGCCCGACCTGTGCGCATCTTCAAGC	378
QY	421	AGATCGTTGAGCCTGAGCGCGGTGATCACTTCCGCGTGTCTGTGCTGAGCAACGCGGCA	480
Db	379	AGATCGTTGAGCCTGAGCGCGGTGATCACTTCCGCGTGTCTGTGCTGAGCAACGCGGCA	438
QY	481	ACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTGTCGCCATCGGCGCTTCAAG	540
Db	439	ACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTGTCGCCATCGGCGCTTCAAG	498
QY	541	GCGGCGTGCAGTCAACCCCTCCGTTGAACTGTCCATCATGAAGTCCCTTGAAGC	600
Db	499	GCGGCGTGCAGTCAACCCCTCCGTTGAACTGTCCATCATGAAGTCCCTTGAAGC	558
QY	601	AGATCTTCAAGAACGCTTGACCAACCTTCCCATAGGCGCGGCAAGGCGGCTCCGACT	660
Db	559	AGATCTTCAAGAACGCTTGACCAACCTTCCCATAGGCGCGGCAAGGCGGCTCCGACT	618
QY	661	TCGACCCCAAGGCGAAGCGCACGCGGAGGTGATGCGCTTCCGAGTCTTCAATGACG	720
Db	619	TCGACCCCAAGGCGAAGCGCACGCGGAGGTGATGCGCTTCCGAGTCTTCAATGACG	678
QY	721	AGCTGCAGCGCACATCAGTACCTGACGAGAGCGTGCAGCGCGGCGGCAATCGGCGTGGCG	780
Db	679	AGCTGCAGCGCACATCAGTACCTGACGAGAGCGTGCAGCGCGGCGGCAATCGGCGTGGCG	738
QY	781	CGCGGAGATTGGCTACCTTTTCGCGCAGTCAAGCGCATCAACAGAACTTACACGCGC	840
Db	739	CGCGGAGATTGGCTACCTTTTCGCGCAGTCAAGCGCATCAACAGAACTTACACGCGC	798
QY	841	TGCTGACCCCGAAGGCGCAGAGATGTGGCGGCTCCGAAATCCGCGCCGAGGCGCACGCGCT	900
Db	799	TGCTGACCCCGAAGGCGCAGAGATGTGGCGGCTCCGAAATCCGCGCCGAGGCGCACGCGCT	858
QY	901	ACGCGCGCGTCTGTTGTGAGAACTGTCTGAAGAACAAAGGCGAGAGCTTCAAGGGCA	960
Db	859	ACGCGCGCGTCTGTTGTGAGAACTGTCTGAAGAACAAAGGCGAGAGCTTCAAGGGCA	918
QY	961	AGCGCTGCTGTGTCTTGCGCGCGGCAACGTGCCCCAGTACTGCGCGGAGTGTCTGTGG	1020
Db	919	AGCGCTGCTGTGTCTTGCGCGCGGCAACGTGCCCCAGTACTGCGCGGAGTGTCTGTGG	978
QY	1021	AGAAAGGCGCATGTGTCTGTTCGCTGTCCGACTCCCAAGGCTACGTGTACGAGGCCAAGC	1080
Db	979	AGAAAGGCGCATGTGTCTGTTCGCTGTCCGACTCCCAAGGCTACGTGTACGAGGCCAAGC	1038
QY	1081	GCTTCAACGCGGAGAGCTGACGAGCGGTGACAGACATGAAGAAAGAAACAACAGCGCC	1140
Db	1039	GCTTCAACGCGGAGAGCTGACGAGCGGTGACAGACATGAAGAAAGAAACAACAGCGCC	1098
QY	1141	GCATCTCCGAGTACAAAGACGACACCGCGGTGTATGTGTGGGACCCGCGCAAGCCTTGGG	1200
Db	1099	GCATCTCCGAGTACAAAGACGACACCGCGGTGTATGTGTGGGACCCGCGCAAGCCTTGGG	1158
QY	1201	AGCTGGAATCTGCAAGGTGACATTCGCTTCCCTCTGCGCCACCCAGAACGATTCGATGAC	1260
Db	1159	AGCTGGAATCTGCAAGGTGACATTCGCTTCCCTCTGCGCCACCCAGAACGATTCGATGAC	1218
QY	1261	ACGACGCGGAGTGTGTATCAAGCAACGCGTGCAGTACGTGTGTGAGGCGCCCAACATGC	1320
Db	1219	ACGACGCGGAGTGTGTATCAAGCAACGCGTGCAGTACGTGTGTGAGGCGCCCAACATGC	1278
QY	1321	CCTCCACCAACGAGGCGCATCCACAGTACAAACAGGCGGCGCATCTTACTGCCCCGCA	1380
Db	1279	CCTCCACCAACGAGGCGCATCCACAGTACAAACAGGCGGCGCATCTTACTGCCCCGCA	1338

QY	1381	AGGAGGCGCAAGCGGGGGGGCTGGCGGGTCAAGCGGCTCGAGATACCGCAGAACCGCATGA	1440
Db	1339	AGGAGGCGCAAGCGGGGGGGCTGGCGGGTCAAGCGGCTCGAGATACCGCAGAACCGCATGA	1398
QY	1441	GCTGAATCTGAACTCGCGAGAGAGTTGCGCGACAACTGGAGCGCATGAAAGACATCT	1500
Db	1399	GCTGAATCTGAACTCGCGAGAGAGTTGCGCGACAACTGGAGCGCATGAAAGACATCT	1458
QY	1501	ACGACTCCGCGCATGGGGCGCTCCCGGAGATACAAATGTGACTGGCTGGCGGCGCCAAACA	1560
Db	1459	ACGACTCCGCGCATGGGGCGCTCCCGGAGATACAAATGTGACTGGCTGGCGGCGCCAAACA	1518
QY	1561	TCGGGGGCTTCACCAAGGTGGCTATCCGCTCAAGGCGCCAGGGCGCTTTAACTGCC	1620
Db	1519	TCGGGGGCTTCACCAAGGTGGCTATCCGCTCAAGGCGCCAGGGCGCTTTAACTGCC	1578
QY	1621	AGGCGCAAGCAGCGCTCAACCGCAATCCAACTCAACCGGCGCAGACCTTTT	1680
Db	1579	AGGCGCAAGCAGCGCTCAACCGCAATCCAACTCAACCGGCGCAGACCTTTT	1638
QY	1661	CGAAGAGCGGGCGCTTTTCCGAGCAGGGCGCTCACTGCGCTTTCAATACCCGCTATT	1740
Db	1639	CGAAGAGCGGGCGCTTTTCCGAGCAGGGCGCTCACTGCGCTTTCAATACCCGCTATT	1698
QY	1741	GCCGCGGTGCCCCCTGCATTTCCACCCGAGAGAACTAGCGGCACTTGACTGCATCAGA	1800
Db	1699	GCCGCGGTGCCCCCTGCATTTCCACCCGAGAGAACTAGCGGCACTTGACTGCATCAGA	1758
QY	1801	CGGCTATTTTTTTTGGCGACGGCGGCTCAACCCGAGAGCTCTCTCCCCGAGCCTTAAGC	1860
Db	1759	CGGCTATTTTTTTTGGCGACGGCGGCTCAACCCGAGAGCTCTCTCCCCGAGCCTTAAGC	1818
QY	1861	GCTGACGTCCCGCCGCACTTTGCTCTCGACATCGCTCGGTTTTGACCCCTTCAGTCTACC	1920
Db	1819	GCTGACGTCCCGCCGCACTTTGCTCTCGACATCGCTCGGTTTTGACCCCTTCAGTCTACC	1878
QY	1921	CACCTGTGTGAAAGCCTACAGCTCAATTGCTTTAATGTATGTGCGGCCCTCTCTGC	1980
Db	1879	CACCTGTGTGAAAGCCTACAGCTCAATTGCTTTAATGTATGTGCGGCCCTCTCTGC	1938
QY	1981	CCCCGAATTTTCCAGCCATGAGAGTGGGGTTCCTAGCCGTGTGACCCCAAGTGTAGCTT	2040
Db	1939	CCCCGAATTTTTCCTGCCATGAGAGTGGGGTTCCTAGCCGTGTGACCCCAAGTGTAGCTT	1998
QY	2041	AGTGTGCGTGCCTTGCCTCTGCGCTGCCCGGAGTGCATCTGTGACCTGAGAGTCTTGT	2100
Db	1999	AGTGTGCGTGCCTTGCCTCTGCGCTGCCCGGAGTGCATCTGTGACCTGAGAGTCTTGT	2058
QY	2101	GTAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA	2140
Db	2059	GTAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA	2098
RESULT 6			
ID	ABK51008	standard; cDNA; 2099 BP.	
AC	ABK51008;		
XX			
XX			
DT	24-SEP-2002	(first entry)	
XX			
DE	cdna encoding NADP-glutamate dehydrogenase beta subunit.		
XX			
KW	NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;		
KW	nitrogen metabolism; plant; ammonium assimilation; transgenic;		
KW	ammonia toxicity tolerance; osmotic stress tolerance; gene; ss-		
XX			
OS	Chlorella sorokiniana.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	33..1571	
FT	/product= "NADP-specific glutamate dehydrogenase beta		

FT subunit
XX US2002062495-A1.
XX 23-MAY-2002.
XX 01-MAY-1998; 98US-00070844.
XX 01-MAY-1998; 98US-00070844.
XX (SCHMIDT R R.
XX (MILLER P.
XX Schmidt RR, Miller P;
XX WPI; 2002-499691/53.
XX P-PSDB; MAU98951.
XX
XX Transforming a plant with a polynucleotide encoding a polypeptide with
XX glutamate dehydrogenase activity provides a plant with modulated nitrogen
XX metabolism useful to increase yield and ammonium and osmotic stress
XX tolerance.
XX
XX Disclosure; Page 15-17; 35pp; English.
XX
XX The invention relates to a method of modulating nitrogen metabolism in
XX plant cells, comprising transforming a plant cell with a polynucleotide
XX encoding a polypeptide having glutamate dehydrogenase activity, and
XX culturing the cell to produce descendant cells which express the
XX polypeptide. The method is used to provide plants with increased yield,
XX improved ammonium assimilation properties, increased tolerance to ammonia
XX toxicity, improved osmotic stress tolerance and improved composition. The
XX present sequence represents the coding sequence of Chlorella sorokiniana
XX NADP-glutamate dehydrogenase beta subunit, used in the method of the
XX invention
XX
XX Sequence 2099 BP; 416 A; 713 C; 616 G; 354 T; 0 U; 0 Other;
XX
XX Query Match 95.6%; Score 2046; DB 6; Length 2099;
XX Best Local Similarity 98.0%; Pred. No. 0;
XX Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
XX
QY 1 CTCCTTTGCTGCGCCCTCTGCTGCGCCGATGCAAGCCGCTGCGCAAGCCTA 60
Db 1 CTCCTTTGCTGCGCCCTCTGCTGCGCCGATGCAAGCCGCTGCGCAAGCCTA 60
QY 61 TCGTGACCGCCCGCTGCGGACCGCCGCGCTGCGCGCTGCGCGCTGCGCGT 120
Db 61 TCGTGACCGCCCGCTGCGGACCGCCGCGCTGCGCGCTGCGCGCTGCGCGT 120
QY 121 TCCGCTCCGCAAGCGCGATGTCGCGCAAGCCGCTGCTGCGTGAAGACAGATCTCG 180
Db 79 TCCGCTCCGCAAGCGCGATGTCGCGCAAGCCGCTGCTGCGTGAAGACAGATCTCG 138
QY 181 CGATGAGCGCAACCGCGGCACTTCAAGCGCGCTGCAAGAGCGGTGAAGCAAGATGCGCA 240
Db 139 CGATGAGCGCAACCGCGGCACTTCAAGCGCGCTGCAAGAGCGGTGAAGCAAGATGCGCA 198
QY 241 CCAAGCGCGGCACTGAGCGCGCTGCAAGCGCGATCAAGACCCGACGTCGCGCAGCTGC 300
Db 199 CCAAGCGCGGCACTGAGCGCGCTGCAAGCGCGATCAAGACCCGACGTCGCGCAGCTGC 258
QY 301 TGACGAGATCTTCAAGAGACCGCGAGACAGAGAGTTCATGAGCGCGGTGCGGAGG 360
Db 259 TGACGAGATCTTCAAGAGACCGCGAGACAGAGAGTTCATGAGCGCGGTGCGGAGG 318
QY 361 TGGCGCTGCTCCGAGCGCGCGTTCGAGAGCGCGCGAGCGTGTGCGCATCTTCAAGC 420
Db 319 TGGCGCTGCTCCGAGCGCGCGTTCGAGAGCGCGCGAGCGTGTGCGCATCTTCAAGC 378
QY 421 AGATGTTGAGCGCTGAGCGCGATCACTTCCGCGTGTCTGCTGAGACGCGCGCA 480
Db 379 AGATGTTGAGCGCTGAGCGCGATCACTTCCGCGTGTCTGCTGAGACGCGCGCA 438

QY 481 ACCTGAGGTCAACCGCGGCTTCCGCGAGTACTGCTCCGCATCGGCCCTTCAAGG 540
Db 439 ACCTGAGGTCAACCGCGGCTTCCGCGAGTACTGCTCCGCATCGGCCCTTCAAGG 498
QY 541 GCGGCTGCGCTTCCACCCCTCCGTGAACCTGTCAATCATAGATTCTTCTTGAGC 600
Db 499 GCGGCTGCGCTTCCACCCCTCCGTGAACCTGTCAATCATAGATTCTTCTTGAGC 558
QY 601 AGATCTTCAAGACAGCTGACACCTGCGCATGAGCGCGGCAAGGCGGCTTCCACT 660
Db 559 AGATCTTCAAGACAGCTGACACCTGCGCATGAGCGCGGCAAGGCGGCTTCCACT 618
QY 661 TCGACCCCAAGGCAAGGCAAGCGGAGGATGCGCTTCCGACGCTTCAATGACG 720
Db 619 TCGACCCCAAGGCAAGGCAAGCGGAGGATGCGCTTCCGACGCTTCAATGACG 678
QY 721 AGCTGACGCGCACAATCAGTACGTGACGAGACGTGCCCGCGGACATCGGCGTGGCG 780
Db 679 AGCTGACGCGCACAATCAGTACGTGACGAGACGTGCCCGCGGACATCGGCGTGGCG 738
QY 781 CGCGGAGATTGCTACTCTTTTGGCCAGTACAAAGCGCATCAAGAACTTACACCGCG 840
Db 739 CGCGGAGATTGCTACTCTTTTGGCCAGTACAAAGCGCATCAAGAACTTACACCGCG 798
QY 841 TGTGACCCCGAAGGCGCAAGAGTATGCGCGCTCCGAGATCCGCGCCGAGCGCACCGGCT 900
Db 799 TGTGACCCCGAAGGCGCAAGAGTATGCGCGCTCCGAGATCCGCGCCGAGCGCACCGGCT 858
QY 901 ACGGCGCGCTGCTTTTGTGAGAACGTGCTGAAGAGCAAGAGGCGAGAGCTTCAAGGCA 960
Db 859 ACGGCGCGCTGCTTTTGTGAGAACGTGCTGAAGAGCAAGAGGCGAGAGCTTCAAGGCA 918
QY 961 AGCGCTGCTGCTGCTGCGCGGCAAGGTGCGCAAGTACTGCGGAGCTGCTGCTG 1020
Db 919 AGCGCTGCTGCTGCTGCGCGGCAAGGTGCGCAAGTACTGCGGAGCTGCTGCTG 978
QY 1021 AGAAGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 979 AGAAGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
QY 1081 GCTTCAAGCGGAGAGCTGAGCGGCTGAGAGCATGAAGAAAGAAAGAAAGAGCGGCC 1140
Db 1039 GCTTCAAGCGGAGAGCTGAGCGGCTGAGAGCATGAAGAAAGAAAGAAAGAGCGGCC 1098
QY 1141 GCATCTCCGAGTACAAAGCGACACCGCGGTGATGATGAGGCGCGCAAGCCTTGGG 1200
Db 1099 GCATCTCCGAGTACAAAGCGACACCGCGGTGATGATGAGGCGCGCAAGCCTTGGG 1158
QY 1201 AGCTGAGTCCGAGTGAATGCGCTTCCCTGCGGCAACCAAGAGATGATGAGC 1260
Db 1159 AGCTGAGTCCGAGTGAATGCGCTTCCCTGCGGCAACCAAGAGATGATGAGC 1218
QY 1261 ACGAGCGGAGCTGCTGATCAAGAGCGGCTGCAAGTACGTGAGAGGCGCCCAATGC 1320
Db 1219 ACGAGCGGAGCTGCTGATCAAGAGCGGCTGCAAGTACGTGAGAGGCGCCCAATGC 1278
QY 1321 CCTCCACCAAGAGGCAATCCAAAGTACAAAGAGCGGCGATCATCTTCTCCCGCA 1380
Db 1279 CCTCCACCAAGAGGCAATCCAAAGTACAAAGAGCGGCGATCATCTTCTCCCGCA 1338
QY 1381 AGGCGGCAATGCGGCGGCTGCGGCTGAGCGGCTGAGATGACCCAGAACCGCATGA 1440
Db 1339 AGGCGGCAATGCGGCGGCTGCGGCTGAGCGGCTGAGATGACCCAGAACCGCATGA 1398
QY 1441 GCTTGAATGAGTCTGAGAGAGGTTGCGCAAGCTGAGAGCGATCATGAAGACATCT 1500
Db 1399 GCTTGAATGAGTCTGAGAGAGGTTGCGCAAGCTGAGAGCGATCATGAAGACATCT 1458
QY 1501 ACGACTCGGCATGAGGCGCTCCGCAAGTACAAAGTGTGACTGCGCGGCGCCAA 1560
Db 1459 ACGACTCGGCATGAGGCGCTCCGCAAGTACAAAGTGTGACTGCGCGGCGCCAA 1518

QY	1561	TCGGGGGCTTACCAAGGTGGCTATGCGTCGAAGGCCAAGGGGCGTSTTAAGCTGCC	1620
Db	1519	TCGGGGGCTTACCAAGGTGGCTATGCGTCGAAGGCCAAGGGGCGTSTTAAGCTGCC	1578
QY	1621	AGGCGCAAGCCACGAGCTCACCGGGCAATCCAAACCCAACTCAAAGCCGACGAGACTTTT	1680
Db	1579	AGGCGCAAGCCACGAGCTCACCGGGCAATCCAAACCCAACTCAAAGCCGACGAGACTTTT	1638
QY	1681	CGAAGCGGGCGCCCTTTTTCACAGCCAGGGCCCTCACTGCGCTTTTCAATAACCTGCTATT	1740
Db	1639	CGAAGCGGGCGCCCTTTTTCACAGCCAGGGCCCTCACTGCGCTTTTCAATAACCTGCTATT	1698
QY	1741	GGCGCGCGGCGCCCTGCAATTCCACCCCAAGAAAGAACTGAGGGGCACTTGACCTGCAATCAGGA	1800
Db	1699	GGCGCGCGGCGCCCTGCAATTCCACCCCAAGAAAGAACTGAGGGGCACTTGACCTGCAATCAGGA	1758
QY	1801	CGGCTATTATTTTTCGCGCAGCGCGGCTCACCCCGAGAGGCTCTCTCCCGAGCCCTAAGC	1860
Db	1759	CGGCTATTATTTTTCGCGCAGCGCGGCTCACCCCGAGAGGCTCTCTCCCGAGCCCTAAGC	1818
QY	1861	GCTGACGTCCGCGCCGACTTTTGCTTCGCAATCGCTCGGTTTTGACCCCTTCAAGTCTAAC	1920
Db	1819	GCTGACGTCCGCGCCGACTTTTGCTTCGCAATCGCTCGGTTTTGACCCCTTCAAGTCTAAC	1878
QY	1921	CACCTGTGTGGAAGCCTAACAGGCTCAATGCTTTTAGTGAATGTGGGCCCCCTCCGCG	1980
Db	1879	CACCTGTGTGGAAGCCTAACAGGCTCAATGCTTTTAGTGAATGTGGGCCCCCTCCGCG	1938
QY	1981	CCCCGAATTTTCTGECATAGACGTCGCGTTCCTAGCTGGTGTGACCCCAAGTAGACAGTT	2040
Db	1939	CCCCGAATTTTCTGECATAGACGTCGCGTTCCTAGCTGGTGTGACCCCAAGTAGACAGTT	1998
QY	2041	AGTGTGCGTGCCTTTCGCTCGCTGCGCTGCGGAGTGGATATCTGTGACTGTGAAGTGCCTTGT	2100
Db	1999	AGTGTGCGTGCCTTTCGCTCGCTGCGCTGCGGAGTGGATATCTGTGACTGTGAAGTGCCTTGT	2058
QY	2101	GTAACAACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140	
Db	2059	GTAACAACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2098	

XX	RESULT 7
AC	AAT64543
ID	AAT64543 standard; cDNA; 2096 BP.
XX	
AC	AAT64543;
XX	
DT	17-OCT-2003 (revised)
DT	10-JUL-1997 (first entry)
XX	
DE	NADP-specific glutamate dehydrogenase beta-subunit precursor cDNA
XX	
KW	Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
XX	chloroplast; transgenic plant; ds.
OS	Chlorella sorokiniana; strain UTEX 1230.
XX	
Key	Location/Qualifiers
FT	CDS 30..1568
FT	/*tag= a
FT	transit_peptide 30..146
FT	/*tag= b
FT	mat_peptide 147..1565
FT	/*tag= c
XX	
PN	MO9712983-A1.
XX	
PD	10-APR-1997.
XX	
PF	03-OCT-1996; 96WO-US015921.
XX	
PR	06-OCT-1995; 95US-00541033.
XX	

Query Match	95.5%	Score 2043	DB 2	Length 2096	
Best Local Similarity	98.0%	Pred. No. 0			
Matches 2095	Conservative	0	Mismatches	0	Indels 42
					Gaps 1
XX PA (UVEL) UNIV FLORIDA.					
XX PI Schmidt RR, Miller P;					
XX DR WP1; 1997-226226/20.					
XX P-PSDB; AAM15408.					
XX PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella					
XX PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism					
XX PT plant cells.					
XX PS Claim 2; Page 41-43; 61pp; English.					
XX CC cDNA clones (AAT64542 and AAT64543) respectively code for the alpha					
CC subunit (AAM15407) and beta subunit (AAM15408) precursor proteins of an					
CC ammonium-inducible, chloroplast-localised NADP-specific glutamate					
CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obtd. by					
CC ligation of 3' clone pBD653 (AAT64531) and 5' clones pGDE63 (AAT64540)					
CC and pGDE64 (AAT64541). The proteins are processed to yield mature alpha					
CC and beta subunits (see also AAT64547-48) that comprise the active NADP-					
CC GDH hexameric isoenzymes. The nitrogen metabolism of plants can be					
CC modulated (pref. by increasing assimilation of inorganic N into organic					
CC N) by transforming them with nucleotide sequences encoding the alpha					
CC and/or beta subunits. Such plants show improved properties, e.g.					
CC increased crop yield and improved stress tolerance. Heteroxemers having					
CC alpha and beta subunits can be expressed that have higher					
CC assimilating/deammonifying activity ratios (i.e. higher capacity for glutamate					
CC synthetase) than homohexamers. (Updated on 17-Oct-2003 to standardise OS					
CC field)					
XX SX Sequence 2096 BP; 416 A; 711 C; 616 G; 353 T; 0 U; 0 Other;					
Query Match	95.5%	Score 2043	DB 2	Length 2096	
Best Local Similarity	98.0%	Pred. No. 0			
Matches 2095	Conservative	0	Mismatches	0	Indels 42
					Gaps 1
QY 4 CTTTCTGTCGCCCTCTCTCCGTCGCCGATGACAGCCGCTCGTCCGCAAGCCTATG 63					
DB 1 CTTTCTGTCGCCCTCTCTCCGTCGCCGATGACAGCCGCTCGTCCGCAAGCCTATG 60					
QY 64 TGGCCGCCCGCTGGCGGACAGCCCGCGCTGCTGCGCGCTGCGCGCTGCGTGGGATCC 123					
DB 61 TGGCC-----TGGCGTGGGATCC 78					
QY 124 GCTCCGCAAGCGCGATGTCGCGGCAAGCCGTCGCTGAGAGACGATCTCCGCA 183					
DB 79 GCTCCGCAAGCGCGATGTCGCGGCAAGCCGTCGCTGAGAGACGATCTCCGCA 138					
QY 184 TGGAGCCACCAACCGCGCATTTCAAGGCGTGCAGAAAGCGGTGAAGCAGATGGCCACGA 243					
DB 139 TGGAGCCACCAACCGCGCATTTCAAGGCGTGCAGAAAGCGGTGAAGCAGATGGCCACGA 198					
QY 244 AGCGCGGACATGAGGGGCTGTGTCACGCGCATCAAGAACCCGACGTCGCCAGCTCTGA 303					
DB 199 AGCGCGGACATGAGGGGCTGTGTCACGCGCATCAAGAACCCGACGTCGCCAGCTCTGA 258					
QY 304 CGAGATCTTCAATGAAGAACCCGAGACAGACAGAGTTCAATGACAGCGGTGCGCGAGGTGG 363					
DB 259 CGAGATCTTCAATGAAGAACCCGAGACAGACAGAGTTCAATGACAGCGGTGCGCGAGGTGG 318					
QY 364 CCGTCTCCTCTGACCGCCGCTGTTGAGAAAGCGCCGAGCTGCTGCCCATTTCAAGACA 423					
DB 319 CCGTCTCCTCTGACCGCCGCTGTTGAGAAAGCGCCGAGCTGCTGCCCATTTCAAGACA 378					
QY 424 TCGTTGAACCTGAGGCGGTGATCACTTCCGCGTCTCCGCTGGAGCGACGCGCGCAAC 483					
DB 379 TCGTTGAACCTGAGGCGGTGATCACTTCCGCGTCTCCGCTGGAGCGACGCGCGCAAC 438					
QY 484 TGCAGGTCAACCGCGGCTTCCGCTGACAGTACTCTGTCGCCCATTCGACCCCTTCAAGGGCG 543					
DB 439 TGCAGGTCAACCGCGGCTTCCGCTGACAGTACTCTGTCGCCCATTCGACCCCTTCAAGGGCG 498					
QY 544 GCTGCGCTTCCACCCCTCCGTAACCTGTCCATCATGAAGTTCTTCTGCTTTGACAGA 603					

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Db 499 GCTGCGCTTCACCCCTCCGTGAACCTGTCATCATGTAAGTTCTTTCCTTTGAGCAGA 558
Qy 604 TCTTCAAGAAAGCTGTACCAACCTGCCCCATGAGGGGGGGCAAGGGGGGGCTTCCACTTGG 663
Db 559 TCTTCAAGAAAGCTGTACCAACCTGCCCCATGAGGGGGGGCAAGGGGGGGCTTCCACTTGG 618
Qy 664 ACCCAAGAGGGAAGAGCAGCGAGGATGATGCGCTTCTGCAAGTCTTTCATGACCGAGC 723
Db 619 ACCCAAGAGGGAAGAGCAGCGAGGATGATGCGCTTCTGCAAGTCTTTCATGACCGAGC 678
Qy 724 TGACGCGGCACATCATGCTACGTCAGAGAGTCCCGCGGCGACATCGCGTGGCGGC 783
Db 679 TGACGCGGCACATCATGCTACGTCAGAGAGTCCCGCGGCGACATCGCGTGGCGGC 738
Qy 784 GCGAGATTGGCTACTCTTTTGGCCAGTACAAAGCATACCAAGAACTACACCGGCTGTC 843
Db 739 GCGAGATTGGCTACTCTTTTGGCCAGTACAAAGCATACCAAGAACTACACCGGCTGTC 798
Qy 844 TGACCCCGAAGGGGCGAGAGTATGGCGGCTCCAGATCCGCGCGGCAACCGGCTACG 903
Db 799 TGACCCCGAAGGGGCGAGAGTATGGCGGCTCCAGATCCGCGCGGCAACCGGCTACG 858
Qy 904 GCGCGCTGCTGTTTGTGAGAGAGTGTGAAGAGCAAGGGGAGAGCTTCAAGGGCAAGC 963
Db 859 GCGCGCTGCTGTTTGTGAGAGAGTGTGAAGAGCAAGGGGAGAGCTTCAAGGGCAAGC 918
Qy 964 GCTGCTGTGTGTCTGAGCGGGGCAAGTGTGCCAGTACTGCGCGGAGTGTCTGTGAGA 1023
Db 919 GCTGCTGTGTGTCTGAGCGGGGCAAGTGTGCCAGTACTGCGCGGAGTGTCTGTGAGA 978
Qy 1024 AGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
Db 979 AGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
Qy 1084 TCACGCGGAGCAGCTGAGGCGGCTGTCAGAGCATGAAAGAAAGAAAGAAAGAGCGCCGCA 1143
Db 1039 TCACGCGGAGCAGCTGAGGCGGCTGTCAGAGCATGAAAGAAAGAAAGAAAGAGCGCCGCA 1098
Qy 1144 TCTCCGAGTACAGAGCAGCACCGCGTGTATGTGTGGGCGACCGCGCAAGCTTTGGAGC 1203
Db 1099 TCTCCGAGTACAGAGCAGCACCGCGTGTATGTGTGGGCGACCGCGCAAGCTTTGGAGC 1158
Qy 1204 TGAGACTGCAAGTGAACATGCGCTTCCCTGCGCACCCAGAAAGAAAGTTCATAGAGCAG 1263
Db 1159 TGAGACTGCAAGTGAACATGCGCTTCCCTGCGCACCCAGAAAGAAAGTTCATAGAGCAG 1218
Qy 1264 AGCGGAGCTGCTGATCAAGCAGCGGCTGCCAGTACGTGTGAGAGGGCGCCCAACATGCCCT 1323
Db 1219 AGCGGAGCTGCTGATCAAGCAGCGGCTGCCAGTACGTGTGAGAGGGCGCCCAACATGCCCT 1278
Qy 1324 CCACCAAGAGGCGCATCCACAAGTACAAAGGCGCGCATCTTACTGCCCGGCAAGG 1383
Db 1279 CCACCAAGAGGCGCATCCACAAGTACAAAGGCGCGCATCTTACTGCCCGGCAAGG 1338
Qy 1384 CCGGCAAGCGCGGCGGCTGCGCGCTCAAGCGGCTTGAAGTGAACCAAGCGCATGAGCC 1443
Db 1339 CCGGCAAGCGCGGCGGCTGCGCGCTCAAGCGGCTTGAAGTGAACCAAGCGCATGAGCC 1398
Qy 1444 TGAAGTGAAGTCCGAGAGGTTCCGCAAGGCTGGAAGCATGAAAGAGCATCTTACG 1503
Db 1399 TGAAGTGAAGTCCGAGAGGTTCCGCAAGGCTGGAAGCATGAAAGAGCATCTTACG 1458
Qy 1504 ACTCGCGCATGAGGCGGCTCCGCAAGTACAAATGTTGACTGTGCGGCGCAACATCG 1563
Db 1459 ACTCGCGCATGAGGCGGCTCCGCAAGTACAAATGTTGACTGTGCGGCGCAACATCG 1518
Qy 1564 CCGGCTTACCAAGTGTGCTGATGCTGCTCAAGGCGCCAGAGGGCTTTTAAGTCCGAG 1623
Db 1519 CCGGCTTACCAAGTGTGCTGATGCTGCTCAAGGCGCCAGAGGGCTTTTAAGTCCGAG 1578
Qy 1624 CCAAGGCAAGGCTTACCGGCAATCCAAAGCAAGCTCAAGGCGAGAGCTTTTGG 1683
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Db 1579 CCAAGCAGCGCTACCGGCAATCCAAAGCAAGCAAGGCGGAGAGCTTTTGG 1638
Qy 1684 AAGGCGGCGCTTTTCCAGCAGAGGCGCTACCGGCGCTTCAATACCTGTATGCG 1743
Db 1639 AAGGCGGCGCTTTTCCAGCAGAGGCGCTACCGGCGCTTCAATACCTGTATGCG 1698
Qy 1744 GCCGTGCGGCTTCAATTCACCCCAAGAGAACTAGGCGGCACTTGTATGATCAGAGCAG 1803
Db 1699 GCCGTGCGGCTTCAATTCACCCCAAGAGAACTAGGCGGCACTTGTATGATCAGAGAGG 1758
Qy 1804 CTATTTTTCGCGACGCGGCTCACCCGAGAGCTCTCTTCCCGAGCCCTAAGCGCT 1863
Db 1759 CTATTTTTCGCGACGCGGCTCACCCGAGAGCTCTCTTCCCGAGCCCTAAGCGCT 1818
Qy 1864 GACGTCGCGGCACTTTTGGCTTGGCAATCGGTGGTTTGAACCCCTCCAGTCAACAC 1923
Db 1819 GACGTCGCGGCACTTTTGGCTTGGCAATCGGTGGTTTGAACCCCTCCAGTCAACAC 1878
Qy 1924 CCTGTTGAGAGCTTACAGCTCAATGCTTTAGTATGATGCGGCGGCTCTGCGCC 1983
Db 1879 CCTGTTGAGAGCTTACAGCTCAATGCTTTAGTATGATGCGGCGGCTCTGCGCC 1938
Qy 1984 CGAATTTTCTGCGATGAGAGCGTGGCTTCTAGCTGTGAGACCCCAAGTACAGTATG 2043
Db 1939 CGAATTTTCTGCGATGAGAGCGTGGCTTCTAGCTGTGAGACCCCAAGTACAGTATG 1998
Qy 2044 GTGCGTGTGCTTGGCTGCGCTGCGGCGGATGCGTATCTGTACCTGAGAGTGTGTGTA 2103
Db 1999 GTGCGTGTGCTTGGCTGCGCTGCGGCGGATGCGTATCTGTACCTGAGAGTGTGTGTA 2058
Qy 2104 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db 2059 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2095

RESULT 8
ID ABR51021
ABR51021 standard; cDNA; 2096 BP.
XX ABR51021;
XX DT 24-SEP-2002 (first entry)
XX DE NADP-glutamate dehydrogenase ligation construct pBGdc53 plus pBGdc64.
XX KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
XX KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
XX KW ammonia toxicity tolerance; osmotic stress tolerance; pBGdc64; pBGdc63;
XX KW gene; ss.
XX OS Chlorella sorokiniana.
XX US2002062495-A1.
XX PD 23-MAY-2002.
XX 01-MAY-1998; 98US-00070844.
XX PR 01-MAY-1998; 98US-00070844.
XX PA (SCHMIDT R. R.
XX PA (MILLER P.
XX PI Schmidt RR, Miller P;
XX DR WPI; 2002-499691/53.
XX PT Transforming a plant with a polynucleotide encoding a polypeptide with
XX PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
XX PT metabolism useful to increase yield and ammonium and osmotic stress
XX PT tolerance.
XX PS Example 2; Page 24-25; 35pp; English.
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XX The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transforming a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants which increase yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance, and improved composition. The
CC present sequence represents the coding sequence of Chlorella sorokiniana
CC NADP-glutamate dehydrogenase. The cloning construct of pBsd65 plus pBsd64,
CC used in the method of the invention

XX Sequence 2096 BP; 416 A; 711 C; 616 G; 353 T; 0 U; 0 Other;

Query Match 95.5%; Score 2043; DB 6; Length 2096;
Best Local Similarity 98.0%; Pred. No. 0; Mismatches 0; Indels 42; Gaps 1;
Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 4 CTTTCTGCTCGCCCTCTCTCCGTCGCCATGACAGCCGCTCTGTCGCAAGCCTATCG 63
DB 1 CTTTCTGCTCGCCCTCTCTCCGTCGCCATGACAGCCGCTCTGTCGCAAGCCTATCG 60
QY 64 TGGCCGCCCCCGCTGCGGCAAGCCCGCTGCTGCGCCGCTGCGCCGCTGCGCTGCGCTCC 123
DB 61 TGGCC-----TGCGCTGCGCTCC 78
QY 124 GCTCCGCAAGCGGATGTCGCGCAAGGCGCTCTGCTGAGAGAGAGATCTCCGGA 183
DB 79 GCTCCGCAAGCGGATGTCGCGCAAGGCGCTCTGCTGAGAGAGAGATCTCCGGA 138
QY 184 TGAAGCGCAACCGCGGCACTTCAAGCGCTGCAAGAGCGGCTGAGAGATGCGCAACA 243
DB 139 TGAAGCGCAACCGCGGCACTTCAAGCGCTGCAAGAGCGGCTGAGAGATGCGCAACA 198
QY 244 AGGCGGCACTGAGAGCGCTGTCGACCGGATCAAGAACCCCGAGTGGCCGCACTGCTGA 303
DB 199 AGGCGGCACTGAGAGCGCTGTCGACCGGATCAAGAACCCCGAGTGGCCGCACTGCTGA 258
QY 304 CCGAGATCTTATGAGAGACCGGAGCAGAGAGATTCATGACAGCGGCTGCGAGGTGG 363
DB 259 CCGAGATCTTATGAGAGACCGGAGCAGAGAGATTCATGACAGCGGCTGCGAGGTGG 318
QY 364 CCGTCTCCCTGACGCGCTGTTGAGAAAGCGCCCGAGCTCTGCCATCTTCAAGAGA 423
DB 319 CCGTCTCCCTGACGCGCTGTTGAGAAAGCGCCCGAGCTCTGCCATCTTCAAGAGA 378
QY 424 TCGTTGAGCTGAGCGCGGTGATCACTTCCGCGTGTCTGCTGAGACAGCGCGCAACC 483
DB 379 TCGTTGAGCTGAGCGCGGTGATCACTTCCGCGTGTCTGCTGAGACAGCGCGCAACC 438
QY 484 TGAAGTCAACCGCGGCTTCCGCGTGAATCTGTCGCCATGAGGCGCCCTCAAGAGGCG 543
DB 439 TGAAGTCAACCGCGGCTTCCGCGTGAATCTGTCGCCATGAGGCGCCCTCAAGAGGCG 498
QY 544 GCGTCCGCTTCCACCCCTCGGTGAACCTGTCCATCATGAGATCTTTCCTTGAAGAGA 603
DB 499 GCGTCCGCTTCCACCCCTCGGTGAACCTGTCCATCATGAGATCTTTCCTTGAAGAGA 558
QY 604 TCTTCAAGAAAGCTGAGCAACCTGCGCAAGGCGGCGCAAGGCGGCTCCGACTTTCG 663
DB 559 TCTTCAAGAAAGCTGAGCAACCTGCGCAAGGCGGCGCAAGGCGGCTCCGACTTTCG 618
QY 664 ACCCAAGGGAAGAGCAGCGGAGGATGATGCGCTTTCGCAAGTCTTTCATGACCGAGC 723
DB 619 ACCCAAGGGAAGAGCAGCGGAGGATGATGCGCTTTCGCAAGTCTTTCATGACCGAGC 678
QY 724 TGAAGCGGCAATGATGATGAGAGAGCGTCCGCGCGGAGCAATCGGCGTGGCGCGC 783
DB 679 TGAAGCGGCAATGATGATGAGAGAGCGTCCGCGCGGAGCAATCGGCGTGGCGCGC 738
QY 784 GCGAGATGAGCTACTTTTGGCGCAGTAAAGCGGATCAACCAAGATCAACCGGCTGCG 843
DB 739 GCGAGATGAGCTACTTTTGGCGCAGTAAAGCGGATCAACCAAGATCAACCGGCTGCG 798

QY 844 TGAACCCGAAGGCGAGAGATATGCGCGCTCCGAGATCCGCCCGAGGCCACCGGCTACG 903
DB 799 TGAACCCGAAGGCGAGAGATATGCGCGCTCCGAGATCCGCCCGAGGCCACCGGCTACG 858
QY 904 GCGCGCTGCTGTTTGTGAGAAAGCTGTGAAGAACAAAGGCGAGAGCTTCAAGGCAAGC 963
DB 859 GCGCGCTGCTGTTTGTGAGAAAGCTGTGAAGAACAAAGGCGAGAGCTTCAAGGCAAGC 918
QY 964 GTCGCTGATGTGCGGCGGAGCAAGTGGCCAGTACTGCGGAGACTCTGCTGAGAGA 1023
DB 919 GTCGCTGATGTGCGGCGGAGCAAGTGGCCAGTACTGCGGAGACTCTGCTGAGAGA 978
QY 1024 AGGCGCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
DB 979 AGGCGCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
QY 1084 TCACGCGGAGAGCTGACGCGGCTGACGAGATGAAAGAAAGAACAAAGCGCGCGCA 1143
DB 1039 TCACGCGGAGAGCTGACGCGGCTGACGAGATGAAAGAAAGAACAAAGCGCGCGCA 1098
QY 1144 TCTCCAGTACAAAGAGGACACCGCGGTATATGAGGCGACCGCGGCAAGCTTGGAGC 1203
DB 1099 TCTCCAGTACAAAGAGGACACCGCGGTATATGAGGCGACCGCGGCAAGCTTGGAGC 1158
QY 1204 TGAAGTCCAGTGTGACATGCGCTTCCCTGCGGCAACCAAGAGATGATGAGCAGC 1263
DB 1159 TGAAGTCCAGTGTGACATGCGCTTCCCTGCGGCAACCAAGAGATGATGAGCAGC 1218
QY 1264 ACGCGAGCTGCTGATTAAGCAAGGCTGCCAGTACGCTGTGAGAGGCGCCAAATGCGCT 1323
DB 1219 ACGCGAGCTGCTGATTAAGCAAGGCTGCCAGTACGCTGTGAGAGGCGCCAAATGCGCT 1278
QY 1324 CCACCAAGAGGCGCATCAACAAGTAAACAAGGCGGCGATCATCTGACCGCGCAAGG 1383
DB 1279 CCACCAAGAGGCGCATCAACAAGTAAACAAGGCGGCGATCATCTGACCGCGCAAGG 1338
QY 1384 CCGGCAACGCGCGGCGGCTGAGCGGCTGAGAGTGAACCCAGAACCGCATGAGCC 1443
DB 1339 CCGGCAACGCGCGGCGGCTGAGCGGCTGAGAGTGAACCCAGAACCGCATGAGCC 1398
QY 1444 TGAAGTGAATCTGCGAGAGAGGCTTGCAGCAAGCTGAGAGCGGCTATTAAGAGATCTTACG 1503
DB 1399 TGAAGTGAATCTGCGAGAGAGGCTTGCAGCAAGCTGAGAGCGGCTATTAAGAGATCTTACG 1458
QY 1504 ACTCCGCAATGAGGCGGCTCCGCGAGATACATGTTGACTGCGTGGCGGCGCAACTCG 1563
DB 1459 ACTCCGCAATGAGGCGGCTCCGCGAGATACATGTTGACTGCGTGGCGGCGCAACTCG 1518
QY 1564 CCGGCTTACCAAGAGTGTGATGCTGCTCAAGGCGGCGGCTGTTAAAGCTTGCAGG 1623
DB 1519 CCGGCTTACCAAGAGTGTGATGCTGCTCAAGGCGGCGGCTGTTAAAGCTTGCAGG 1578
QY 1624 CCGAAGCAAGGCTCACCGGCAATCAACCAACCACTCAAGCGGCGAGAGCTTTCGCG 1683
DB 1579 CCGAAGCAAGGCTCACCGGCAATCAACCAACCACTCAAGCGGCGAGAGCTTTCGCG 1638
QY 1684 AAGCGGCGCTTTCACGAGGCGGCTCACTGCGCTTTCATTAACCTGCTATTTGCC 1743
DB 1639 AAGCGGCGCTTTCACGAGGCGGCTCACTGCGCTTTCATTAACCTGCTATTTGCC 1688
QY 1744 GCGTGGCCCTGCAATTCACCCCAAGAAAGCTGAGGAGCACTTGAATGATGAGAGCG 1803
DB 1699 GCGTGGCCCTGCAATTCACCCCAAGAAAGCTGAGGAGCACTTGAATGATGAGAGCG 1758
QY 1804 CTATTTTTCGCGAGCGCGGCTTCAACCGGAGGCTCTTCCCGGAGGCTTAAAGGCT 1863
DB 1759 CTATTTTTCGCGAGCGCGGCTTCAACCGGAGGCTCTTCCCGGAGGCTTAAAGGCT 1818
QY 1864 GAGTCCGCGGCACTTTCGCTGCGACATGCTGCTGTTTGAACCCCTCCAGTCTTACCCAC 1923
DB 1819 GAGTCCGCGGCACTTTCGCTGCGACATGCTGCTGTTTGAACCCCTCCAGTCTTACCCAC 1878

QY 1924 CCTGTTGGAAGCCTACAGCCTAATGCTTTAGTGTGATGTGGCCCCCTCTGCCCC 1983
 DB 1879 CTTGTTGGAAGCCTACAGCCTAATGCTTTAGTGTGATGTGGCCCCCTCTGCCCC 1938
 QY 1984 GGAATTTTCTGTCATGAGAGCGTGGCTTCTAGCTGTGAGACCCCAAGTACAGTAACT 2043
 DB 1939 CGAATTTTCTGTCATGAGAGCGTGGCTTCTAGCTGTGAGACCCCAAGTACAGTAACT 1998
 QY 2044 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2103
 DB 1999 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2058
 QY 2104 AACACGACGAGTCAAAAAA 2140
 DB 2059 AACACGACGAGTCAAAAAA 2095
 RESULT 9
 ADQ36706 ID ADQ36706 standard; cDNA, 2124 BP.
 AC ADQ36706;
 DT 23-SEP-2004 (first entry)
 XX
 DE NADP-specific GDH alpha subunit precursor protein cDNA, SEQ ID 1.
 KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
 KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase;
 KW gene; ss.
 XX Chlorella sorokiniana.
 OS
 XX Key Location/Qualifiers
 FT CDS 33..1613
 FT /tag= a
 FT /product= "NADP-specific GDH alpha subunit precursor
 FT protein"
 XX US2004128710-A1.
 PD 01-JUL-2004.
 XX
 PF 24-JUL-2003; 2003US-00627886.
 XX
 PR 01-MAY-1998; 98US-00070844.
 XX
 PA (SCHMIDT R. R.
 PA (MILLER P.
 XX
 PI Schmidt RR, Miller P;
 XX
 DR WPI: 2004-53134/51.
 DR P-PSDB; ADQ36707.
 XX
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant
 PT with increased yield and improved tolerance to ammonia toxicity and
 PT osmotic stress, by transforming plant cell with nucleic acid having
 PT glutamate dehydrogenase activity.
 XX
 PS Disclosure; SEQ ID NO 1; 36pp; English.
 XX
 CC The present invention relates to increasing or decreasing the nitrogen
 CC metabolism in plant cells by transforming a plant cell with a
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
 CC ADQ36731), or their fragments, which exhibits GDH activity. The
 CC polynucleotide is operably linked to a polynucleotide encoding a
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
 CC fragments that exhibit chloroplast transit activity. The method is useful
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The
 CC methods, polynucleotides, and polypeptides are useful in producing plant

CC with increased yield, and with improved tolerance to ammonia toxicity,
 CC osmotic stress, and composition of the crop or plant. The present
 CC sequence is the coding sequence for the precursor protein of the alpha
 CC subunit of the NADP-specific GDH, which is then processed to produce the
 CC mature alpha subunit of the NADP-specific GDH, used in the method of the
 CC invention.
 XX
 SQ Sequence 2124 BP; 413 A; 730 C; 629 G; 352 T; 0 U; 0 Other;
 Query Match 95.3%; Score 2040; DB 12; Length 2124;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 2124; Conservative 0; Mismatches 0; Indels 14; Gaps 7;
 QY 1 CTCCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 DB 1 CTCCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 QY 61 TCGTGGCCGCGCCGCTGAGCGGCAAGCCGCGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 120
 DB 61 TCGTGGCCGCGCCGCTGAGCGGCAAGCCGCGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 120
 QY 121 TCGGCTCCGCGCAAGCGGATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGATCTTCG 180
 DB 121 TCGGCTCCGCGCAAGCGGATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGATCTTCG 180
 QY 181 CGATGAGAGCGCCACACCGCGCATCTTACAGCGCGCTGCGAGAAAGCGGTGAAGATGCGCA 240
 DB 181 CGATGAGAGCGCCACACCGCGCATCTTACAGCGCGCTGCGAGAAAGCGGTGAAGATGCGCA 240
 QY 241 CCAAGCGCGGCACTGAGAGCGCGTGTGACAGCGCATCAAGAACCCCGAGCGTGGCCAGCTGC 300
 DB 241 CCAAGCGCGGCACTGAGAGCGCGTGTGACAGCGCATCAAGAACCCCGAGCGTGGCCAGCTGC 300
 QY 301 TGAACGAGATCTTATGAGAGACCCGAGACAGAGAGATTCATGACAGCGGTGCGCGAG 360
 DB 301 TGAACGAGATCTTATGAGAGACCCGAGAGAGAGATTCATGACAGCGGTGCGCGAG 360
 QY 361 TGGCGGTCTCCCTGACGCGCGGTGTTGAGAAAGCGCCCGAGCTGCTGCTTCAAGC 420
 DB 361 TGGCGGTCTCCCTGACGCGCGGTGTTGAGAAAGCGCCCGAGCTGCTGCTTCAAGC 420
 QY 421 AGATCGTTGAGCGTGAAGCGCGGTATCACTTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 421 AGATCGTTGAGCGTGAAGCGCGGTATCACTTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 481 ACTGCAAGTCAACCGCGGCTTCGCGGTGCAAGTCTGCTGCGCATGCGCCCTTACAAG 540
 DB 481 ACTGCAAGTCAACCGCGGCTTCGCGGTGCAAGTCTGCTGCGCATGCGCCCTTACAAG 540
 QY 541 GCGGCTGCGCTTCAACCCCTCCGTGAACCTGTCAATCAATGAACTTTCCTTGAAGC 600
 DB 541 GCGGCTGCGCTTCAACCCCTCCGTGAACCTGTCAATCAATGAACTTTCCTTGAAGC 600
 QY 541 GCGGCTGCGCTTCAACCCCTCCGTGAACCTGTCAATCAATGAACTTTCCTTGAAGC 600
 DB 541 GCGGCTGCGCTTCAACCCCTCCGTGAACCTGTCAATCAATGAACTTTCCTTGAAGC 600
 QY 601 AGATCTTCAAGAACAGCGCTGACACCGTGCATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
 DB 601 AGATCTTCAAGAACAGCGCTGACACCGTGCATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
 QY 661 TCGACCCCAAGGCGGAGAGCGAGCGGAGGATGCGCTTCTGCAATGACG 720
 DB 661 TCGACCCCAAGGCGGAGAGCGAGCGGAGGATGCGCTTCTGCAATGACG 720
 QY 721 AGCTGACGCGGCATACGCTACGTCGAGAGAGTGTGCGCGCGCGGCGGCGGCGGCGGCGGCGG 780
 DB 721 AGCTGACGCGGCATACGCTACGTCGAGAGAGTGTGCGCGCGCGGCGGCGGCGGCGGCGGCGG 780
 QY 781 CGGCGGAGATTTGCTACCTTTTGGCGAGTCAAGGCGCATCAACCAAGATCAACCGGCGG 840
 DB 781 CGGCGGAGATTTGCTACCTTTTGGCGAGTCAAGGCGCATCAACCAAGATCAACCGGCGG 840
 QY 841 TGTGACCCCGAAGGCGGAGAGTATGCGGCTTCCGATCCGCGCGGAGCGGCGGCGGCGGCGGCT 900
 DB 841 TGTGACCCCGAAGGCGGAGAGTATGCGGCTTCCGATCCGCGCGGAGCGGCGGCGGCGGCGGCT 900

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Qy 901 ACAGGCGCGTCTGTTTGTGAGAACTGTGTAAGGACAAAGGCGAGAGCCTCAAGGCA 960
Db 901 ACAGGCGCGTCTGTTTGTGAGAACTGTGTAAGGACAAAGGCGAGAGCCTCAAGGCA 960
Qy 961 AGCGTGTCTGTGTCTGTGCGCGGCAACGTGGCCAGTACTGGCGGAGCTGCTGTGG 1020
Db 961 AGCGTGTCTGTGTCTGTGCGCGGCAACGTGGCCAGTACTGGCGGAGCTGCTGTGG 1020
Qy 1021 AGAAGGCGCGCATGTGTGTGTGCGGTGCGAATCCCAAGGCTACGTGTACAGGCGCAAG 1080
Db 1021 AGAAGGCGCGCATGTGTGTGTGCGGTGCGAATCCCAAGGCTACGTGTACAGGCGCAAG 1080
Qy 1081 GCTTCAACGCGGAGAGCTGCAAGGCGGTGCAAGACATGAGAAAGAAACAAACAGCGCC 1140
Db 1081 GCTTCAACGCGGAGAGCTGCAAGGCGGTGCAAGACATGAGAAAGAAACAAACAGCGCC 1140
Qy 1141 GCATCTCCGAGTACAAAGGCAACCGCGGTGTATGTGTGGGAGACCGCGCAAGCTTGGG 1200
Db 1141 GCATCTCCGAGTACAAAGGCAACCGCGGTGTATGTGTGGGAGACCGCGCAAGCTTGGG 1200
Qy 1201 AGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGGCGCACCCAGAACGAGATCGATGAGC 1260
Db 1201 AGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGGCGCACCCAGAACGAGATCGATGAGC 1260
Qy 1261 ACAGAGCGGAGCTGTGTATCAAGCAAGGCTGCGAGTACGTGTGAGGCGCCCAACATGC 1320
Db 1261 ACAGAGCGGAGCTGTGTATCAAGCAAGGCTGCGAGTACGTGTGAGGCGCCCAACATGC 1320
Qy 1321 CCTCCACCAAGAGGAGCTTCCCAAGTACAAAGGCGGAGTATCTATCTGCCCCGCA 1380
Db 1321 CCTCCACCAAGAGGAGCTTCCCAAGTACAAAGGCGGAGTATCTATCTGCCCCGCA 1380
Qy 1381 AGGCGGCGCAAGCGCGCGCGGTGCGGTGCGAGCGGCTGAGANTGACCCAGAACGCAATGA 1440
Db 1381 AGGCGGCGCAAGCGCGCGCGGTGCGGTGCGAGCGGCTGAGANTGACCCAGAACGCAATGA 1440
Qy 1441 GCCTGAACCTGAGCTGCGAGGAGGTTGCGCAACAGCTGAGAGGATCATGAAAGGCAATCT 1500
Db 1441 GCCTGAACCTGAGCTGCGAGGAGGTTGCGCAACAGCTGAGAGGATCATGAAAGGCAATCT 1500
Qy 1501 ACAGACTCCGCGCATGGGGCGGTCCGCAATATCAATGTGTGACTGTGGCTGGCGGCCAACA 1560
Db 1501 ACAGACTCCGCGCATGGGGCGGTCCGCAATATCAATGTGTGACTGTGGCTGGCGGCCAACA 1560
Qy 1561 TCGCGGCGCTTCAACCAAGGTGCTGATGCGTCAAGGCGCCAGGCGCTGTTTAAAGTGGCC 1620
Db 1561 TCGCGGCGCTTCAACCAAGGTGCTGATGCGTCAAGGCGCCAGGCGCTGTTTAAAGTGGCC 1620
Qy 1621 AGGCGCGCAAGCGGCTCACCGGCAATCAACCCAACTCAACGCGCCAGAACCTTTT 1680
Db 1621 AGGCGCGCAAGCGGCTCACCGGCAATCAACCCAACTCAACGCGCCAGAACCTTTT 1680
Qy 1681 CGGAAGCGGCGCTTTTCCAGCGCAAGGCGCTCACTGCCCCCTTTCATTAACCTGCAATTT 1740
Db 1681 CGGAAGCGGCGCTTTTCCAGCGCAAGGCGCTCACTGCCCCCTTTCATTAACCTGCAATTT 1740
Qy 1741 GCCGCGCGCTGCGCAATTTCAACCCCAAGAAAGAACTGAGCGCACTTACTGATCAAGAA 1800
Db 1741 GCCGCGCGCTGCGCAATTTCAACCCCAAGAAAGAACTGAGCGCACTTACTGATCAAGAA 1800
Qy 1801 CGGCTATTTTTTTCGCGACGCGCGCTCAACCCGAGAGGCTCTTCCCGGAGAGCCTTAAGC 1860
Db 1801 CGGCTATTTTTTTCGCGACGCGCGCTCAACCCGAGAGGCTCTTCCCGGAGAGCCTTAAGC 1860
Qy 1861 GCTGACGTGCGCGCGCACTTTTGCCTGCGACATGCTGCTGTTTGAACCCCTCAAGTAAAC 1920
Db 1861 GCTGACGTGCGCGCGCACTTTTGCCTGCGACATGCTGCTGTTTGAACCCCTCAAGTAAAC 1920
Qy 1921 CACCTGTGTGAGAGCTACCAAGCTCAATGCTTTTATGTATGTGAGCGCCCTCCGCGC 1980
Db 1921 CACCTGTGTGAGAGCTACCAAGCTCAATGCTTTTATGTATGTGAGCGCCCTCCGCGC 1980
Qy 1981 CCGCGAATTTTTCTGCGCATGAGACGTGCGGTTCTTACGCTGTGACCCCAAGTAGCAATT 2040

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Db 1971 CCGCGAATTTTCTGCGCA--AGACGTGCGGTCTTACGCTGTGACCCCAAGTAGCAATT 2028
Qy 2041 AGTGTGCGTCCCTTGGCGGCGTCCCGGAGTACGATCTGTGACCTGAGAGTCTGT 2100
Db 2029 AGTGTGCGTCCCTTGGCGGCGTCCCGGAGTACGATCTGTGACCTGAGAGTCTGT 2086
Qy 2101 GTAAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2138
Db 2087 GTAAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2124

RESULT 10
AAT64531
ID AAT64531 standard; cDNA; 1969 BP.
XX
AC AAT64531;
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
DE Glutamate dehydrogenase cDNA clone pBSPc53.
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KM chloroplast; transgenic plant; ds.
XX
OS Chlorella sorokiniana; strain UTEX 1230.
XX
PN M09712983-A1.
XX
PD 10-APR-1997.
XX
PF 03-OCT-1996; 96MO-US015921.
XX
PR 06-OCT-1995; 95US-00541033.
XX
PA (UFL) UNIV FLORIDA.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 1997-226226/20.
XX
PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
XX
PS Claim 2; Page 35-36; 61pp; English.
XX
CC A cDNA clone (AAT64531), designated pBSPc53, was isolated from a
CC Chlorella sorokiniana cDNA library in lambda ZAP by screening with an
CC NADP-specific glutamate dehydrogenase (NADP-GDH) cDNA probe. It comprises
CC the complete 3'-terminal region of the C. sorokiniana NADP-GDH sequence.
CC 5' terminal regions were obtd. by PCR, yielding full-length clones
CC (AAT64542-43) for the alpha and beta subunits of C. sorokiniana NADP-GDH.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1969 BP; 401 A; 659 C; 580 G; 329 T; 0 U; 0 Other;

Query Match 92.0%; Score 1969; DB 2; Length 1969;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 CAGATCTCCGAGTGAAGCAGCACCACCGGCACTTCAAGCGCGCTGACAGAGCGGTGAAG 230
Db 1 CAGATCTCCGAGTGAAGCAGCACCACCGGCACTTCAAGCGCGCTGACAGAGCGGTGAAG 60
Qy 231 CAGATGCGCACCAAGGCGGCACTGAGGCGCTGTGTCACGCGCATCAAGAACCCCGACGTG 290
Db 61 CAGATGCGCACCAAGGCGGCACTGAGGCGCTGTGTCACGCGCATCAAGAACCCCGACGTG 120
Qy 291 CGGAGCTGCTGACCGCAGATCTTTCATGAAGACCCGAGACGACGAGATTTCATGCAAGCG 350
Db 121 CGGAGCTGCTGACCGCAGATCTTTCATGAAGACCCGAGACGAGATTTCATGCAAGCG 180

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QY 351 GTGCGGAGGTGGCGGTCTCCCTGCGAGCCCGGTGTTGAGAGAGCGCCCGAGCTGTGCCC 410
 DB 181 GTGCGGAGGTGGCGGTCTCCCTGCGAGCCCGGTGTTGAGAGAGCGCCCGAGCTGTGCCC 240
 QY 411 ATCTTCAAGAGATGTTGAGCGCTGAGCGCGTGATCACTTCCGCGTGTCTGCTGAGC 470
 DB 241 ATCTTCAAGAGATGTTGAGCGCTGAGCGCGTGATCACTTCCGCGTGTCTGCTGAGC 300
 QY 471 GAGCGCGGCAACCTGCAAGTCAACCGCGCGCTTCCCGGTGCAATCTGCTCCGCACTCCGC 530
 DB 301 GAGCGCGGCAACCTGCAAGTCAACCGCGCGCTTCCCGGTGCAATCTGCTCCGCACTCCGC 360
 QY 531 CCCTTCAAGAGCGCGCTGCGCTTCCACCCCTCCGGAACCTGTCCATGATGAAGTTCTT 590
 DB 361 CCCTTCAAGAGCGCGCTGCGCTTCCACCCCTCCGGAACCTGTCCATGATGAAGTTCTT 420
 QY 591 GCCTTGAAGAGATCTTCAAGAACAGCTGACCACTGCGCCATGAGCGCGCGCAAGGCG 650
 DB 421 GCCTTGAAGAGATCTTCAAGAACAGCTGACCACTGCGCCATGAGCGCGCGCAAGGCG 480
 QY 651 GCGTCCGACTTGCAGCCCAAGGCGCAAGCGCGAGGTGATGCGCTTCTGCGCACTCC 710
 DB 481 GCGTCCGACTTGCAGCCCAAGGCGCAAGCGCGAGGTGATGCGCTTCTGCGCACTCC 540
 QY 711 TTCAATGACCGAGCTGCAAGCGCGCAATCACTGAGAGACGTGCGCGCGCGCGCAATC 770
 DB 541 TTCAATGACCGAGCTGCAAGCGCGCAATCACTGAGAGACGTGCGCGCGCGCGCAATC 600
 QY 771 GCGCTGAGCGCGCGCGAGATTGCTACTTTTCGCGCAGTACCAAGCGCATCAACAGAAC 830
 DB 601 GCGCTGAGCGCGCGCGAGATTGCTACTTTTCGCGCAGTACCAAGCGCATCAACAGAAC 660
 QY 831 TACACCGGCGTGTGACCCCGAAGGCGCAAGATGCGCGCTCCGAGATCCGCCGAG 890
 DB 661 TACACCGGCGTGTGACCCCGAAGGCGCAAGATGCGCGCTCCGAGATCCGCCGAG 720
 QY 891 GCGACCGGCTACCGGCGCGCTGTTTGTGAGAACGTGCTGAAGAGAACAGGCGAGAGC 950
 DB 721 GCGACCGGCTACCGGCGCGCTGTTTGTGAGAACGTGCTGAAGAGAACAGGCGAGAGC 780
 QY 951 CTCAAGGCGCAAGCGCTGCTGTGTCTGCGCGCGCAACGTGCGCCAGTACTGCGCGAG 1010
 DB 781 CTCAAGGCGCAAGCGCTGCTGTGTCTGCGCGCGCAACGTGCGCCAGTACTGCGCGAG 840
 QY 1011 CTGCTGCTGAGAAAGGCGCGCATGTGTGTGCTGTGCTGCACTGCCAGGCGTACGTGAC 1070
 DB 841 CTGCTGCTGAGAAAGGCGCGCATGTGTGTGCTGTGCTGCACTGCCAGGCGTACGTGAC 900
 QY 1071 GAGCGCAACGGGCTTCAACCGCGAGAGCTGAGAGCGGTGCGAGACATGAGAGAGAAC 1130
 DB 901 GAGCGCAACGGGCTTCAACCGCGAGAGCTGAGAGCGGTGCGAGACATGAGAGAGAAC 960
 QY 1131 AACAGCGCGCGCATCTCCGAGTACCAAGAGCAACCGCGGTATGTGGGCGACCGCGCG 1190
 DB 961 AACAGCGCGCGCATCTCCGAGTACCAAGAGCAACCGCGGTATGTGGGCGACCGCGCG 1020
 QY 1191 AAGCTTGAAGAGCTGAGCTGCGAGTGAATGCGCTTCCCTGCGCGCACCCAGAACGAG 1250
 DB 1021 AAGCTTGAAGAGCTGAGCTGCGAGTGAATGCGCTTCCCTGCGCGCACCCAGAACGAG 1080
 QY 1251 ATCGATGAGACGACGCGCGAGCTGTGTATCAAGACGCGCGTCCAGTATGTGTGAGGCG 1310
 DB 1081 ATCGATGAGACGACGCGCGAGCTGTGTATCAAGACGCGCGTCCAGTATGTGTGAGGCG 1140
 QY 1311 GCGCAACATGCGCTTCCAGCAAGAGCGCATCCAGAGTACCAAGAGCGCGGATCATCTAC 1370
 DB 1141 GCGCAACATGCGCTTCCAGCAAGAGCGCATCCAGAGTACCAAGAGCGCGGATCATCTAC 1200
 QY 1371 TGCGCGGCAAGGCGCGCGCAACGCGCGCGGTGCGGTCAAGCGCGCTGAGATGACCCAG 1430
 DB 1201 TGCGCGGCAAGGCGCGCGCAACGCGCGCGGTGCGGTCAAGCGCGCTGAGATGACCCAG 1260

QY 1431 AACCGCATGAGCGCTGAACCTGAGACTCGGAGAGAGGTTGCGCAAGAGCTGAGCGCATATG 1490
 DB 1261 AACCGCATGAGCGCTGAACCTGAGACTCGGAGAGAGGTTGCGCAAGAGCTGAGCGCATATG 1320
 QY 1491 AAGACATCTACGACTCGCGCATGAGGCGCGTCCCGCAGATACAAATGTTGACTGTGCGG 1550
 DB 1321 AAGACATCTACGACTCGCGCATGAGGCGCGTCCCGCAGATACAAATGTTGACTGTGCGG 1380
 QY 1551 GCGCGCAACATCGGCGGCTTCAACGAGGTGCTATGCGCGTCAAGCGCCAGGCGGCTGT 1610
 DB 1381 GCGCGCAACATCGGCGGCTTCAACGAGGTGCTATGCGCGTCAAGCGCCAGGCGGCTGT 1440
 QY 1611 TAAGCTGCCAGGCGCCCAAGCCAGCGCTCAACGCGCATCAACCCAACTCAACGCGCC 1670
 DB 1441 TAAGCTGCCAGGCGCCCAAGCCAGCGCTCAACGCGCATCAACCCAACTCAACGCGCC 1500
 QY 1671 AGAACCTTTTGGAAAGCGCGCGCTTTTTCAGGCGAGGCGCTCACTGCGCTTTCATTA 1730
 DB 1501 AGAACCTTTTGGAAAGCGCGCGCTTTTTCAGGCGAGGCGCTCACTGCGCTTTCATTA 1560
 QY 1731 CCTGCTATTTGCGCGCGCTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAC 1790
 DB 1561 CCTGCTATTTGCGCGCGCTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCACTTGAC 1620
 QY 1791 TGCAATCAAGAGCGCTATTTTTCGCGAGCGCGCTCACCCCGAGAGCGCTCTCCCGG 1850
 DB 1621 TGCAATCAAGAGCGCTATTTTTCGCGAGCGCGCTCACCCCGAGAGCGCTCTCCCGG 1680
 QY 1851 AGCCCTAAGCGCTGACGTCGCGCGCGACTTTCCTGCAATCGCTCGGTTTGAACCCCT 1910
 DB 1681 AGCCCTAAGCGCTGACGTCGCGCGCGACTTTCCTGCAATCGCTCGGTTTGAACCCCT 1740
 QY 1911 CCACTTACCCAGCGCTGTTGTAAGAGCTCAAGCTCAATTCCTTTTATGATGTGCGC 1970
 DB 1741 CCACTTACCCAGCGCTGTTGTAAGAGCTCAAGCTCAATTCCTTTTATGATGTGCGC 1800
 QY 1971 CCCCTCGCGCGCGCGAAATTTTCTGCGCATGAGAGTGGGTTCTTAGCTGTGACCCCA 2030
 DB 1801 CCCCTCGCGCGCGCGAAATTTTCTGCGCATGAGAGTGGGTTCTTAGCTGTGACCCCA 1860
 QY 2031 AGTAGAGTTAGTGTGCGCTTTCCTGCGCTGCGCTGCGCGGATGCGATCTGTGACCTGA 2090
 DB 1861 AGTAGAGTTAGTGTGCGCTTTCCTGCGCTGCGCTGCGCGGATGCGATCTGTGACCTGA 1920
 QY 2091 GAGTCTTGTGTAAACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2139
 DB 1921 GAGTCTTGTGTAAACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 1969

RESULT 11
 ABR5109
 ID ABR5109 standard; cDNA; 1969 BP.
 XX
 AC ABR5109;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE NADP-glutamate dehydrogenase clone pBdpc53.
 XX
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
 KW ammonia toxicity tolerance; osmotic stress tolerance; pBdpc53; gene; ss.
 OS Chlorella sorokiniana.
 XX
 PN US2002062495-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 01-MAY-1998; 98US-00070844.
 XX
 PR 01-MAY-1998; 98US-00070844.
 XX

PA (SCHM/) SCHMIDT R. R.
PA (MILL/) MILLER P.
PI Schmidt RR, Miller P;
XX WPI: 2002-499691/53.
XX
XX Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
PT tolerance.
XX
XX Example 2; Page 19-20; 35pp; English.
XX
XX The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transforming a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants with increased yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the coding sequence of Chlorella sorokiniana
CC NADP-glutamate dehydrogenase clone pGd53, used in the method of the
CC invention
XX
SQ Sequence 1969 BP; 401 A; 659 C; 580 G; 329 T; 0 U; 0 Other;
Query Match 92.0%; Score 1969; DB 6; Length 1969;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 171 CAGATCTCCGAGTGAAGCGCACCGGCGATTCAAGCGCTGACAGAGCGGTGAAG 230
DB 1 CAGATCTCCGAGTGAAGCGCACCGGCGATTCAAGCGCTGACAGAGCGGTGAAG 60
OY 231 CAGATGCGCACCAAGCGGCGCACTGAGGGGCTGTGTGACGCGCATCAAGAACCCGACGTG 290
DB 61 CAGATGCGCACCAAGCGGCGCACTGAGGGGCTGTGTGACGCGCATCAAGAACCCGACGTG 120
OY 291 CGCGAGCTGTGACCGAGATCTTCATGAAAGACCGGAGACGAGAAATTGATGAGGCG 350
DB 121 CGCGAGCTGTGACCGAGATCTTCATGAAAGACCGGAGACGAGAAATTGATGAGGCG 180
OY 351 GTGCGCGAGGTGCGCTCTCCCTGCGAGCCGCTGTGAGAAAGCGCCGAGCTGTGCGC 410
DB 181 GTGCGCGAGGTGCGCTCTCCCTGCGAGCCGCTGTGAGAAAGCGCCGAGCTGTGCGC 240
OY 411 ATCTTCAAGCAGATGTTGAGCGCTGAGCGCGTGTACCTTCCGCGTCTGTGCTGAGC 470
DB 241 ATCTTCAAGCAGATGTTGAGCGCTGAGCGCGTGTACCTTCCGCGTCTGTGCTGAGC 300
OY 471 GAGCGCGGCAACCTGCAAGTCAACCGGCGCTTCCGCGTGCATCTCGTCCGCAATCGGC 530
DB 301 GAGCGCGGCAACCTGCAAGTCAACCGGCGCTTCCGCGTGCATCTCGTCCGCAATCGGC 360
OY 531 CCTTCAAGAGGCGGCTCGCTTCCAGCCCTCCGGAACCTGTCCATGATGAAGTTCCTT 590
DB 361 CCTTCAAGAGGCGGCTCGCTTCCAGCCCTCCGGAACCTGTCCATGATGAAGTTCCTT 420
OY 591 GCGTTTGAAGCAGATCTTCAAGAACGCTGACCACTTCCCATGAGGCGGCGGCAAGGCG 650
DB 421 GCGTTTGAAGCAGATCTTCAAGAACGCTGACCACTTCCCATGAGGCGGCGGCAAGGCG 480
OY 651 GCGTCCGACTTGCAGCCCAAGGCAAGGCGAGCGGAGGTGATGCGTTTGTCCAGTCC 710
DB 481 GCGTCCGACTTGCAGCCCAAGGCAAGGCGAGCGGAGGTGATGCGTTTGTCCAGTCC 540
OY 711 TTCAATGACGAGCTGAGCGGCAATGAGTGAAGAGAGTGCAGCGGCGGCGGCAATC 770
DB 541 TTCAATGACGAGCTGAGCGGCAATGAGTGAAGAGAGTGCAGCGGCGGCGGCAATC 600
OY 771 GCGGTGCGCGCGCGGAGATTGCTACTTTTCGCGCAGTACAAAGCGCATCAAGAAC 830
|||||

DB 601 GCGGTGCGCGCGCGGAGATTGCTACTTTTCGCGCAGTACAAAGCGCATCACCAAGAAC 660
OY 831 TACACCGGCGGTGAGTACCCCGAAGGGCGCAGAGATGAGCGGCTCCGATCCGCCCGAG 890
DB 661 TACACCGGCGGTGAGTACCCCGAAGGGCGCAGAGATGAGCGGCTCCGATCCGCCCGAG 720
OY 891 GCCACCGGCTTACCGCGCGGCTGTTTGTGAGAACGTGTGAGAACCAAGGCGGAGAGC 950
DB 721 GCCACCGGCTTACCGCGCGGCTGTTTGTGAGAACGTGTGAGAACCAAGGCGGAGAGC 780
OY 951 CTCAAGGCGCAAGCGCTGCTGTGTGTGTGCGGCGGCAAGTGTGCCCATCTGTGCGCGAG 1010
DB 781 CTCAAGGCGCAAGCGCTGCTGTGTGTGTGCGGCGGCAAGTGTGCCCATCTGTGCGCGAG 840
OY 1011 CTGCTGTGAGAAAGGGCGGCGCATGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1070
DB 841 CTGCTGTGAGAAAGGGCGGCGCATGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 900
OY 1071 GAGCCCAACGGCTTTCAGCGCGGAGCAGCTGAGCGGTGAGGACATGAAGAAAGAAC 1130
DB 901 GAGCCCAACGGCTTTCAGCGCGGAGCAGCTGAGCGGTGAGGACATGAAGAAAGAAC 960
OY 1131 AACAGCGCCGCGCATCTCCGAGTACAGAGGAGCAACCGCCGTGTATGTGTGGCGACCCGCC 1190
DB 961 AACAGCGCCGCGCATCTCCGAGTACAGAGGAGCAACCGCCGTGTATGTGTGGCGACCCGCC 1020
OY 1191 AAGCTTGGGAGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGTGCGCACCCAGAACAG 1250
DB 1021 AAGCTTGGGAGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGTGCGCACCCAGAACAG 1080
OY 1251 ATCGATGAGCAAGCGCGGAGCTGTGATCAAGCAGCGCTGTGCGCATGCTGTGTGAGGCG 1310
DB 1081 ATCGATGAGCAAGCGCGGAGCTGTGATCAAGCAGCGCTGTGCGCATGCTGTGTGAGGCG 1140
OY 1311 GCCAACATGCGCTTCAACCAAGAGGCAATCCCAAGTACAAAGAGCGGCGCATCTTAC 1370
DB 1141 GCCAACATGCGCTTCAACCAAGAGGCAATCCCAAGTACAAAGAGCGGCGCATCTTAC 1200
OY 1371 TGCCCGGCAAGGGCGGCGCAACCGCGGCGGTGTGAGCGGCTGTGAGATGACCCAG 1430
DB 1201 TGCCCGGCAAGGGCGGCGCAACCGCGGCGGTGTGAGCGGCTGTGAGATGACCCAG 1260
OY 1431 AACCGATGAGCTGAACTGGAATCGGAGAGAGTTGCGCAAGAGCTGTGAGCGCATATG 1490
DB 1261 AACCGATGAGCTGAACTGGAATCGGAGAGAGTTGCGCAAGAGCTGTGAGCGCATATG 1320
OY 1491 AAGGACATCTACGACTCGGCTGATGAGGCGCTCCCGGAGATACAAATGTTGACCTGTGCGC 1550
DB 1321 AAGGACATCTACGACTCGGCTGATGAGGCGCTCCCGGAGATACAAATGTTGACCTGTGCGC 1380
OY 1551 GCGCGCAACATCGGCGGCTTCAACCAAGTGTGATGCGCTCAAGGCGCCAGGCGCTGTT 1610
DB 1381 GCGCGCAACATCGGCGGCTTCAACCAAGTGTGATGCGCTCAAGGCGCCAGGCGCTGTT 1440
OY 1611 TAACTGCGCAAGGCGCCCAAGCGGCTCACCGGCAATCAACCCCAACCACTCAAGCGGC 1670
DB 1441 TAACTGCGCAAGGCGCCCAAGCGGCTCACCGGCAATCAACCCCAACCACTCAAGCGGC 1500
OY 1671 AGGACCTTTTTCGAAAGGCGGCGCTTTTTCGAGCGCAAGGCGGCTTCACTGCGCTTTCATTA 1730
DB 1501 AGGACCTTTTTCGAAAGGCGGCGCTTTTTCGAGCGCAAGGCGGCTTCACTGCGCTTTCATTA 1560
OY 1731 CCCGTATTGCGCGCGTGCCTTGCAGATTCAACCCCAAGAGAACTAGGCGGCACTTGAC 1790
DB 1561 CCCGTATTGCGCGCGTGCCTTGCAGATTCAACCCCAAGAGAACTAGGCGGCACTTGAC 1620
OY 1791 TGCAATGAGAGCGGCTATTTTTCGAGCGCGCTCAACCCCAAGAGAGCTTCTCCCGC 1850
DB 1621 TGCAATGAGAGCGGCTATTTTTCGAGCGCGCTCAACCCCAAGAGAGCTTCTCCCGC 1680
OY 1851 AGCCCTAAGGCGTGAAGTCCGCGGAGCTTTTGTGCTGTGCAATGCTGTGTTTGAACCCCT 1910
DB 1681 AGCCCTAAGGCGTGAAGTCCGCGGAGCTTTTGTGCTGTGCAATGCTGTGTTTGAACCCCT 1740
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QY 1911 CCAAGTCTACCAACCTGTTGTAAGCTTCAATGCTTTAGTATGAGC 1970
 DB 1741 CCAAGTCTACCAACCTGTTGTAAGCTTCAATGCTTTAGTATGAGC 1800
 QY 1971 CCCCTCTGCCCCGCAATTTTCTCTGCAATGAGCGTGGTCTTAGCTGTGACCCA 2030
 DB 1801 CCCCTCTGCCCCGCAATTTTCTCTGCAATGAGCGTGGTCTTAGCTGTGACCCA 1860
 QY 2031 AGTAGCAATTAATGATGCTGCTTCCCTGCGCTGCGCGGATGCGATCTGTACCTGA 2090
 DB 1861 AGTAGCAATTAATGATGCTGCTTCCCTGCGCTGCGCGGATGCGATCTGTACCTGA 1920
 QY 2091 GAGTCTGTTGTAACAGCAGAGCTCAAAAAA 2139
 DB 1921 GAGTCTGTTGTAACAGCAGAGCTCAAAAAA 1969
 RESULT 12
 ADQ36708
 ID ADQ36708 standard; cDNA; 2083 BP.
 AC ADQ36708;
 DT 23-SEP-2004 (first entry)
 XX
 DE NADP-specific GDH beta subunit precursor protein cDNA, SEQ ID 3.
 XX
 KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
 KW beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase;
 KW gene; ss.
 XX
 OS Chlorella sorokiniana.
 XX
 FH Key Location/Qualifiers
 FT CDS 33..1571
 FT /tag= a
 FT /product= "NADP-specific GDH beta subunit precursor
 FT protein"
 XX
 PN US2004128710-A1.
 XX
 PD 01-JUL-2004.
 XX
 PE 24-JUL-2003; 2003US-00627886.
 XX
 PR 01-MAY-1998; 98US-00070844.
 PA (SCHMIDT R R.
 PA (MILLER P.
 PI Schmidt RR, Miller P;
 XX
 XX WPI; 2004-533134/51.
 DR P-PSDB; ADQ36709.
 XX
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant
 PT with increased yield and improved tolerance to ammonia toxicity and
 PT osmotic stress, by transforming plant cell with nucleic acid having
 PT glutamate dehydrogenase activity.
 XX
 PS Disclosure; SEQ ID NO 3; 36pp; English.
 XX
 CC The present invention relates to increasing or decreasing the nitrogen
 CC metabolism in plant cells by transforming a plant cell with a
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
 CC ADQ36731), or their fragments, which exhibits GDH activity. The
 CC polynucleotide is operably linked to a polynucleotide encoding a
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
 CC fragments that exhibit chloroplast transit activity. The method is useful
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The

CC method, polynucleotides, and polypeptides are useful in producing plant
 CC with increased yield, and with improved tolerance to ammonia toxicity,
 CC osmotic stress, and composition of the crop or plant. The present
 CC sequence is the coding sequence for the precursor protein of the beta
 CC subunit of the NADP-specific GDH, which is then processed to produce the
 CC mature alpha subunit of the NADP-specific GDH, used in the method of the
 CC invention.
 SQ Sequence 2083 BP; 415 A; 709 C; 611 G; 348 T; 0 U; 0 Other;
 Query Match 90.5%; Score 1935.8; DB 12; Length 2083;
 Best Local Similarity 97.1%; Pred. No. 1e-310;
 Matches 2076; Conservative 0; Mismatches 7; Indels 56; Gaps 8;
 QY 1 CTCCTTTTGTGCTGCGCTCTTCTCCGTCCCGCATGACAGACCGCCCTGTGCGCAAGCTTA 60
 DB 1 CTCCTTTTGTGCTGCGCTCTTCTCCGTCCCGCATGACAGACCGCCCTGTGCGCAAGCTTA 60
 QY 61 TCGTGGCCGCCCGCTGGCGGCAAGCGCGCTGCTGCGCGTGGCCGCGTGGG 120
 DB 61 TCGTGGCC-----TGGCGTGGG 78
 QY 121 TCGCTCGCCAGCGCGAGTTCGCGCAAGCGCGTCTGCTGAGAGAGATCTTCG 180
 DB 79 TCGCTCGCCAGCGCGAGTTCGCGCAAGCGCGTCTGCTGAGAGAGATCTTCG 138
 QY 181 CGATGAGAGCCCAACCGCGGCACTTTCACGCGGTGCGAAGGCGGTGAAGATGGCCA 240
 DB 139 CGATGAGAGCCCAACCGCGGCACTTTCACGCGGTGCGAAGGCGGTGAAGATGGCCA 198
 QY 241 CCAAGCGCGGCACTGAGGCGCTGGTGCACGGCATCAAGAACCCGACGTGCGCCAGCTGC 300
 DB 199 CCAAGCGCGGCACTGAGGCGCTGGTGCACGGCATCAAGAACCCGACGTGCGCCAGCTGC 258
 QY 301 TGAACGAGATCTTATGAGAGACCCGAGACAGAGATTATCAAGCGGTGCGCGAG 360
 DB 259 TGAACGAGATCTTATGAGAGACCCGAGAGAGAGATTATCAAGCGGTGCGCGAG 318
 QY 361 TGGCGGTCTCTCTGACAGCGGTGTTCAAGAACCGCGGAGCTGCTGCCATCTTCAAGC 420
 DB 319 TGGCGGTCTCTCTGACAGCGGTGTTCAAGAACCGCGGAGCTGCTGCCATCTTCAAGC 378
 QY 421 AGATCGTTGAGCGTGAAGCGGTGATCACTTCGCGGTGCTGCTGAGAGAGCGCGCA 480
 DB 379 AGATCGTTGAGCGTGAAGCGGTGATCACTTCGCGGTGCTGCTGAGAGAGCGCGCA 438
 QY 481 ACTGCAAGTCAACCGCGGTTCGCGTGAAGTACTGCTCGCCATCGGCCCTTACAAG 540
 DB 439 ACTGCAAGTCAACCGCGGTTCGCGTGAAGTACTGCTCGCCATCGGCCCTTACAAG 498
 QY 541 GCGGCTGCGCTTCAACCCCTCGGTGAACCTGTCAATGAGATTCTTGCCTTGAAGC 600
 DB 499 GCGGCTGCGCTTCAACCCCTCGGTGAACCTGTCAATGAGATTCTTGCCTTGAAGC 558
 QY 601 AGATCTTCAAGAACAGCTGACCAACCTGCGCATGAGCGGCGCAAGGCGGCTCCGACT 660
 DB 559 AGATCTTCAAGAACAGCTGACCAACCTGCGCATGAGCGGCGCAAGGCGGCTCCGACT 618
 QY 661 TCGACCCCAAGGAGGAG 720
 DB 619 TCGACCCCAAGGAGGAG 678
 QY 721 AGCTGACAGCGGCACATGACTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 679 AGCTGACAGCGGCACATGACTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738
 QY 781 CGGCGAGATTGGTACTTTTGGGCGAGTGAAGAGGAGATCAACCAAGATCAACCGGCG 840
 DB 739 CGGCGAGATTGGTACTTTTGGGCGAGTGAAGAGGAGATCAACCAAGATCAACCGGCG 798
 QY 841 TGCTGACCCCAAGGAGGAG 900
 DB 799 TGCTGACCCCAAGGAGGAG 858

OY	901	10GGGCGCCGTCCTGTTTTCGTGGAGAACGTCGTGAAGAGAAACAAGGCGAGAGCCTCCAAAGGCA	960
Db	859	ACGGGCGCGTCTGTTTGTGGAGAACGTGTGAAAGAGAAACAAGGCGAGAGCCTCCAAAGGCA	918
OY	961	AGCGCTGCTCTGTGTCTTGCGCGCGGAGCAACGTGGCCCACTAGTACGTGCGCGAGAGCTGTGCTGTG	1020
Db	919	AGCGCTGCTCTGTGTCTTGCGCGCGGAGCAACGTGGCCCACTAGTACGTGCGCGAGAGCTGTGCTGTG	978
OY	1021	AGAAAGGCGCCATCGTGTCTGTTCGTCTGTCCGACTCCCAAGGCTACGTGTATCGAGGCCCAACG	1080
Db	979	AGAAAGGCGCCATCGTGTCTGTTCGTCTGTCCGACTCCCAAGGCTACGTGTATCGAGGCCCAACG	1038
OY	1081	GCTTACACGCGAGAGAGCTGCAAGGCGGTGACAGACATGAAGAAAGAAACAACAGCGCC	1140
Db	1039	GCTTACACGCGCGAGAGAGCTGCAAGGCGGTGACAGACATGAAGAAAGAAACAACAGCGCC	1098
OY	1141	GCATCTCCGAGTACAAAGACGACACCGCGGTGTATGTGGCGGACCGCGCAAGCCTTGGG	1200
Db	1099	GCATCTCCGAGTACAAAGACGACACCGCGGTGTATGTGGCGGACCGCGCAAGCCTTGGG	1158
OY	1201	AGCTGGACTGGCAGGTGTGACATCGCTTCCCTGTGGGACACCGAAGAGATTCGATGAGC	1266
Db	1159	AGCTGGACTGGCAGGTGTGACATCGCTTCCCTGTGGGACACCGAAGAGATTCGATGAGC	1218
OY	1261	ACGACGCGGAGCTGTGATTCAAAGCAAGGCTGTGCATGACGTGGTGAAGGCGCCCAACATGC	1320
Db	1219	ACGACGCGGAGCTGTGATTCAAAGCAAGGCTGTGCATGACGTGGTGAAGGCGCCCAACATGC	1278
OY	1321	CCTCCACCAACGAGAGCCCATCCACAAAGTACAAACAAGGCGGCACTATCTATCTGCCCCGCA	1380
Db	1279	CCTCCACCAACGAGAGCCCATCCACAAAGTACAAACAAGGCGGCACTATCTATCTGCCCCGCA	1338
OY	1381	AGGCGGCGCAACGCGCGCGGCGGTGCGGTACAGGCGGCTGAGATGACCCGAGAACCGCATGA	1440
Db	1339	AGGCGGCGCAACGCGCGCGGCGGTGCGGTACAGGCGGCTGAGATGACCCGAGAACCGCATGA	1398
OY	1441	GCTTGAACCTGCACTTCGCGAGAGAGTTGCGGACAAAGCTGAGCGCATCTGAAAGACATCT	1500
Db	1399	GCTTGAACCTGCACTTCGCGAGAGAGTTGCGGACAAAGCTGAGCGCATCTGAAAGACATCT	1458
OY	1501	ACGATCCGCGCAATGGGCGCGTCCGCGCAATACAAATGTTGACCTGGCTGCGGAGCGCAACA	1560
Db	1459	ACGATCCGCGCAATGGGCGCGTCCGCGCAATACAAATGTTGACCTGGCTGCGGAGCGCAACA	1518
OY	1561	TCGCGGAGCTTCAACCAAGGTGGCTGATGCGCTCAAGGCGCCAGGCGCGCTTTTAAAGTGGCC	1620
Db	1519	TCGCGGAGCTTCAACCAAGGTGGCTGATGCGCTCAAGGCGCCAGGCGCGCTTTTAAAGTGGCC	1578
OY	1621	AGGCCCAAGCCACGGCTCAACGGGCAATCCAAACCAACACACACACACACACACACACACCTTTT	1680
Db	1579	AGGCCCAAGCCACGGCTCAACGGGCAATCCAAACCAACACACACACACACACACACACCTTTT	1638
OY	1681	CGGAAGCGGCGCTTTTCCAGCGAGGAGCCTCACTGCGCTTTCATAAACCTGTGCTAT	1740
Db	1639	CGGAAGCGGCGCTTTTCCAGCGAGGAGCCTCACTGCGCTTTCATAAACCTGTGCTAT	1698
OY	1741	GCCGCGCTGCCCCCTGCATATCCACCCCAAGAAAGTACGCGGCACTTGACTGTGCATCAGGA	1800
Db	1697	GCCGCGCTGCCCCCTGCATATCCACCCCAAGAAAGTACGCGGCACTTGACTGTGCATCAGGA	1754
OY	1801	CGGCTATTTTTCGCGAGCGCGGCTCAACCCGAGAGGCTCTCTCCCGAGGCGCTTAAGC	1860
Db	1755	CGGCTATTTTTCGCGAGCGCGGCTCAACCCGAGAGGCTCTCTCCCGAGGCGCTTAAGC	1812
OY	1861	GCTGACGTTCGCGCGGACTTGTGCTGTGCAACATGCTCGGTTTTTGAACCCCTCCAGTCTAC	1920
Db	1813	GCTGACGTTCGCGCGGACTTGTGCTGTGCAACATGCTCGGTTTTTGAACCCCTCCAGTCTAC	1870
OY	1921	CACCTGTGTGTGAACCTTACAGCTCAATGCTCTTTTATGTGTATGTGGCCCCCTCTCTGC	1980
Db	1871	CACCTGTGTGTGAACCTTACAGCTCAATGCTCTTTTATGTGTATGTGGCCCCCTCTCTGC	1928

QY	1961	UCCCGAATTTTCCTCCGCAATGAGAGCTGGCTTCTTACGCTGGTACCCCAAGTGCAGTT	2040
Db	1929	CCCCGA--TTCCCTGCACATGAGAGTGGCTTCTTACCTGGTACCCCAAGTGCAGTT	1986
QY	2041	AGTGTGCGTGCCTTGCCTGGCTGGCTGCCGGAGTCGATACCTGTACCTGAGAGTGTGT	2100
Db	1967	AGTGTGC--GCCTTGCCTTGCCTGGCTGGCTGCCGGATCGATACCTGTACCTGAGAGTGTGT	2044
QY	2101	GTAAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAA	2139
Db	2045	GTAAACACCGAGTCAAAAAAAAAAAAAAAAAAAAAA	2083
RESULT 13			
ADQ36723	ID	ADQ36723 standard; cDNA; 2084 BP.	
AC	ADQ36723;		
XX			
XX	23-SEP-2004 (first entry)		
XX			
DE	Full-length NADP-GDH cDNA clone, SEQ ID 18.		
XX			
XX	Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;		
KM	NADP-specific GDH; NADP-specific glutamate dehydrogenase; ss.		
XX	Chlorella sorokiniana.		
XX	US2004128710-A1.		
PN			
XX	01-JUL-2004.		
PD			
XX	24-JUL-2003; 2003US-00627886.		
PF			
XX	01-MAY-1998; 98US-00070844.		
PR			
XX	(SCHM/) SCHMIDT R R.		
PA	(MILL/) MILLER P.		
XX			
PI	Schmidt RR, Miller P;		
XX			
PS	WPI, 2004-533134/51.		
XX			
XX	Example 2; SEQ ID NO 18; 36pp; English.		
CC			
CC	The present invention relates to increasing or decreasing the nitrogen		
CC	metabolism in plant cells by transforming a plant cell with a		
CC	polynucleotide encoding a polypeptide having glutamate dehydrogenase		
CC	(GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH		
CC	(ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,		
CC	ADQ36731), or their fragments, which exhibits GDH activity. The		
CC	polynucleotide is operably linked to a polynucleotide encoding a		
CC	chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their		
CC	fragments that exhibit chloroplast transit activity. The method is useful		
CC	for increasing or decreasing the nitrogen metabolism in plant cells. The		
CC	method, polynucleotides, and polypeptides are useful in producing plant		
CC	cells with increased yield, and with improved tolerance to ammonia toxicity,		
CC	osmotic stress, and composition of the crop or plant. The present		
CC	invention is a cDNA clone which was isolated during the isolation of the		
CC	NADP-specific GDH cDNAs of the invention. Ten NADP-GDH clones were		
CC	identified in an example from the invention. Sequence analysis revealed		
CC	all ten clones were identical at their 3' termini and differed by varying		
CC	degrees of truncation at their 5' termini. Clone pBGD53 (ADQ36712) was		
CC	the longest clone and was found to have a complete 3' terminus, but was		
CC	not long enough to encode either NADP-GDH subunit and so PCR was carried		
CC	out to determine the 5' terminal sequence using primers ADQ36713-ADQ36717		
CC	and ADQ36720, resulting in isolation of the 5' cDNA clones pBGDC 60		
CC	(ADQ36718), pBGDC 61 (ADQ36719), pBGDC 63 (ADQ36721) and pBGDC 64		

CC (ADQ36722) and the full-length clones ADQ36723 and ADQ36724.
XX Sequence 2084 BP; 407 A; 711 C; 614 G; 352 T; 0 U; 0 Other;

Query Match 79.0%; Score 1691; DB 12; Length 2084;
Best Local Similarity 97.5%; Pred. No. 2,8e-270;
Matches 2084; Conservative 0; Mismatches 0; Indels 53; Gaps 34;

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QY 4. CTTTCTGTCGCGCCCTCTCCGCTCCGCGCATGACAGACCGCCCTGCTCCGCAAGCTTATCG 63
DB 1 CTTTCTGTCGCGCCCTCTCTCCGCTCCGCGCATGACAGACCGCCCTGCTCCGCAAGCTTATCG 60
QY 64 TGGCCGCGCCGCTGGCGGCAACGCGCGCTGCTGCGCGCGGCGCGTGGCGGTGGTCC 123
DB 61 TGGCCGCGCCGCTGGCGGCAACGCGCGCTGCTGCGCGCGGCGCGTGGCGGTGGTCC 119
QY 124 GCTCCGCAAGCGCGATGTCGCGCGCAAGCGCGTCTGCTGGAGGAGAGATCTCCGCA 183
DB 120 GCTCCGCAAGCGCGATGTCGCGCGCAAGCGCGTCTGCTGGAGGAGAGATCTCCGCG- 178
QY 184 TGGAGCGCAACCGCGCGATCTTACGCGCGCTGCGAGAGCGGTGAAGAGATGCGACCA 243
DB 179 TGGAGCGCAACCGCGCGATCTTACGCGCGCTGCGAGAGCGGTGAAGAGATGCGACCG- 237
QY 244 AGGCGGCGCACTGAGGCGCGGTGTCAGCGGATCAAGAACCGCGAGCGCGTGGTCTGA 303
DB 238 AGGCGGCGCACTGAGGCGCGGTGTCAGCGGATCAAGAACCGCGAGCGCGTGGTCTG- 296
QY 304 CCGAGATCTTATGAGAGACCGCGAGCAGCAGAGATTCAGAGCGGTGCGCGAGTGG 363
DB 297 CCGAGATCTTATGAGAGACCGCGAGCAGCAGAGATTCAGAGCGGTGCGCGAGTGG- 355
QY 364 CCGTCTCCCTGAGCGCGCTGTCGAGAGACCGCGAGCTGCTGCCATCTTCAAGCAGA 423
DB 356 CCGTCTCCCTGAGCGCGCTGTCGAGAGACCGCGAGCTGCTGCCATCTTCAAGCAG- 414
QY 424 TCGTTGAGCTGAGGCGCGGTGATCACTTCGCGGTGTCGCGGTGAGCAGCGCGGCAAC 483
DB 415 TCGTTGAGCTGAGGCGCGGTGATCACTTCGCGGTGTCGCGGTGAGCAGCGCGGCAAC- 473
QY 484 TGCAGGTCAACCGCGGCTTCGCGGTGAGTACGTCGCGCATTCGCGCCCTTACAGAGGCG 543
DB 474 TGCAGGTCAACCGCGGCTTCGCGGTGAGTACGTCGCGCATTCGCGCCCTTACAGAGGCG- 532
QY 544 GCGTGCCTTCCACCCCTTCGCGTGAACCTGTGCATATGAAGTTCTTCCCTTTGAGCAGA 603
DB 533 GCGTGCCTTCCACCCCTTCGCGTGAACCTGTGCATATGAAGTTCTTCCCTTTGAGCAG- 591
QY 604 TCTTCAAGAGAGCTGACACCCCTGCGCATGCGCGGCGGCAAGGCGGCTCCGACTTCG 663
DB 592 TCTTCAAGAGAGCTGACACCCCTGCGCATGCGCGGCGGCAAGGCGGCTCCGACTTC- 650
QY 664 ACCCGAAGGAGAGAGCAGCGAGGAGTATGCGCTTTCGCGAGTCTTTCATGACGAGC 723
DB 651 ACCCGAAGGAGAGAGCAGCGAGGAGTATGCGCTTTCGCGAGTCTTTCATGACGAG- 709
QY 724 TGCAGCGCGCATATGACTAGTGCAGAGAGTGCCTCCGCGCGACATTCGCGGTGGCGGC 783
DB 710 TGCAGCGCGCATATGACTAGTGCAGAGAGTGCCTCCGCGCGACATTCGCGGTGGCGGC- 768
QY 784 GCGAGATTGGCTACTCTTTTGGCGCGATCAAGCGGATCAACCAAGAACTACACCGGCTGC 843
DB 769 GCGAGATTGGCTACTCTTTTGGCGCGATCAAGCGGATCAACCAAGAACTACACCGGCGTG- 827
QY 844 TGACCCCGAAGGAGAGAGTATGCGCGCTCCGAGATCCGCGCGAGCGCAACGCGCTACG 903
DB 828 TGACCCCGAAGGAGAGAGTATGCGCGCTCCGAGATCCGCGCGAGCGCAACGCGCTAC- 886
QY 904 GCGCGCTGCTGTTTGGAGAGAGCTGTGAAGAGCAGAGGCGAGAGCTTCAAGGCGCAAGC 963
DB 887 GCGCGCTGCTGTTTGGAGAGAGCTGTGAAGAGCAGAGGCGAGAGCTTCAAGGCGCAAG- 945
QY 964 GCTGCTGCTGCTGCTGCGCGGCAACGTCGCCAGTACTGCGCGGAGAGTCTGCTGAGAGA 1023
```

```
DB 946 GCTGCTGCTGCTGCTGCGCGGCGGCAACGTCGCCAGTACTGCGCGGAGGCTGCTGCTG--GA 1003
QY 1024 AGGCGCGCATGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083
DB 1004 AGGCGCGCATGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1061
QY 1084 TCAGCGCGAGCAGCTGAGCGCGGTGCGAGCAGTGAAGAAAGAAAGAAAGCGCGCGCA 1143
DB 1062 TCAGCGCGAGCAGCTGAGCGCGGTGCGAGCAGTGAAGAAAGAAAGAAAGCGCGCGCG-- 1119
QY 1144 TCTCCGAGTACAGAGCAGCAGCCCGCTGTATGTGCGCGAGCCGCGCAAGCTTGGAGC 1203
DB 1120 TCTCCGAGTACAGAGCAGCAGCCCGCTGTATGTGCGCGAGCCGCGCAAGCTTGGAG-- 1177
QY 1204 TGGACTGCGAGTGAATCGCTCTTCCCTGCGCGCACCCAGAGCAGATGATGAGCAGC 1263
DB 1178 TGGACTGCGAGTGAATCGCTCTTCCCTGCGCGCACCCAGAGCAGATGATGAGCAGC-- 1235
QY 1264 ACGCGAGCTGCTGATCAAGAGCGGCTGCGAGTACGTCGAGAGGCGCGCAAGTCCCT 1323
DB 1236 ACGCGAGCTGCTGATCAAGAGCGGCTGCGAGTACGTCGAGAGGCGCGCAAGTCCCT-- 1293
QY 1324 CCACCAAGAGGCGCATCCACAGTACAAAGAGCGCGCATCTATCTGCGCGCGCAAG 1383
DB 1294 CCACCAAGAGGCGCATCCACAGTACAAAGAGCGCGCATCTATCTGCGCGCGCAAG-- 1351
QY 1384 CGGCGCAAGCGCGCGCGTGGCGGTGTCAGCGGCTGAGAGTACCGAGAACCGCATAGCC 1443
DB 1352 CGGCGCAAGCGCGCGCGTGGCGGTGTCAGCGGCTGAGAGTACCGAGAACCGCATAGG-- 1409
QY 1444 TGAATGGAATCTGCGAGAGAGTTCGCGCAAGCTGAGCGGATCATGAAGAGCATCTACG 1503
DB 1410 TGAATGGAATCTGCGAGAGAGTTCGCGCAAGCTGAGCGGATCATGAAGAGCATCTA-- 1467
QY 1504 ACTCGCGCATGAGGCGCGCTCCGCGAGTACATGTTGACTGCGCGGCGCGCAAGTACG 1563
DB 1468 ACTCGCGCATGAGGCGCGCTCCGCGAGTACATGTTGACTGCGCGGCGCGCAAGTAC-- 1525
QY 1564 CGGCGCTTCCAGAGTGGCTGATGCTGTCAGAGCGCGCGAGGCGCTGTTTAACTGCGCAG 1623
DB 1526 CGGCGCTTCCAGAGTGGCTGATGCTGTCAGAGCGCGCGAGGCGCTGTTTAACTGCGCAG-- 1583
QY 1624 CCAGAGCAGCGCTCACCGGCAATCCAGACCACTCAAGCGCGCAGAGCTTTTGG 1683
DB 1584 CCAGAGCAGCGCTCACCGGCAATCCAGACCACTCAAGCGCGCAGAGCTTTTTC-- 1641
QY 1684 AAGGCGCGCTTTTCCAGAGCAGGCGCTGACCTGCGCTTCAPAACCCGCTATTGCC 1743
DB 1642 AAGGCGCGCTTTTCCAGAGCAGGCGCTGACCTGCGCTTCAPAACCCGCTATTGCC-- 1699
QY 1744 GCGGTGCGCTGCAATTCACCCCAAGAGAGTATGCGGCGCACTGATGATCAGAGCG 1803
DB 1700 GCGGTGCGCTGCAATTCACCCCAAGAGAGTATGCGGCGCACTGATGATCAGAGCG-- 1757
QY 1804 CTATTTTTCGCGAGCGCGGCTCACCCCGAGAGCTTCTCCCGAGGCGCTTAAAGCGCT 1863
DB 1758 CTATTTTTCGCGAGCGCGGCTCACCCCGAGAGCTTCTCCCGAGGCGCTTAAAGCG-- 1815
QY 1864 GACGTCGCGCGGCTGCTGCGCGAGCATGCGTGGTTTGAACCGCTCCAGTCAACCGAC 1923
DB 1816 GACGTCGCGCGGCTGCTGCGCGAGCATGCGTGGTTTGAACCGCTCCAGTCAACCGAC-- 1873
QY 1924 CCGTGTGAGAGCTTACAGCTCAATGCTTTTATGATGATGAGCGCGCGCTCTGCGCCC 1983
DB 1874 CCGTGTGAGAGCTTACAGCTCAATGCTTTTATGATGATGAGCGCGCGCTCTGCG--CC 1931
QY 1984 CGAATTTTCTGCGCATGAGAGTGGGTTCTTACCTGCTGAGACCCCAAGTACAGTTAGT 2043
DB 1932 CGAATTTTCTGCGCATGAGAGTGGGTTCTTACCTGCTGAGACCCCAAGTACAGTTAG-- 1989
QY 2044 GTGCGTGCCTTGGCGCTGCGCGCGGAGTGCATCTGAGAGCTGAGAGTCTGAGTGA 2103
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Db 1990 GTGCGTGGCTTGGCCCTGGCGCTCCCGGATCGACTACTGACTGAGAGTCTTG-- 2047
Qy 2104 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2140
Db 2048 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAA 2084
RESULT 14
ADQ36724
ID ADQ36724 standard; cDNA; 2045 BP.
XX ADQ36724;
XX
XX ADQ36724;
XX
XX 23-SEP-2004 (first entry)
XX
XX Full-length NADP-GDH cDNA clone, SEQ ID 19.
XX
XX Nitrogen metabolism, plant; glutamate dehydrogenase; GDH; enzyme;
XX NADP-specific GDH; NADP-specific glutamate dehydrogenase; ss.
XX Chlorella sorokiniana.
XX
XX US2004128710-A1.
XX
XX 01-JUL-2004.
XX
XX 24-JUL-2003; 2003US-00627886.
XX
XX 01-MAY-1998; 98US-00070844.
XX
XX (SCHM/) SCHMIDT R R.
XX (MILL/) MILLER P.
XX
XX Schmidt RR, Miller P;
XX
XX WPI: 2004-533134/51.
XX
XX
XX Increasing or decreasing nitrogen metabolism in plant cells, for plant
XX with increased yield and improved tolerance to ammonia toxicity and
XX osmotic stress, by transforming plant cell with nucleic acid having
XX glutamate dehydrogenase activity.
XX
XX
XX Example 2; SEQ ID NO 19; 36bp; English.
XX
XX The present invention relates to increasing or decreasing the nitrogen
XX metabolism in plant cells by transforming a plant cell with a
XX polynucleotide encoding a polypeptide having glutamate dehydrogenase
XX (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
XX (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
XX ADQ36731), or their fragments, which exhibits GDH activity. The
XX polynucleotide is operably linked to a polynucleotide encoding a
XX chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
XX fragments that exhibit chloroplast transit activity. The method is useful
XX for increasing or decreasing the nitrogen metabolism in plant cells. The
XX methods, polynucleotides, and polypeptides are useful in producing plant
XX with increased yield, and with improved tolerance to ammonia toxicity,
XX osmotic stress, and composition of the crop or plant. The present
XX sequence is a cDNA clone which was isolated during the isolation of the
XX NADP-specific GDH cDNAs of the invention. Ten NADP-GDH clones were
XX identified in an example from the invention. Sequence analysis revealed
XX all ten clones were identical at their 3' termini and differed by varying
XX degree of truncation at their 5' termini. Clone pBGDC53 (ADQ36712) was
XX the longest clone and was found to have a complete 3' terminus, but was
XX not long enough to encode either NADP-GDH subunit and so PCR was carried
XX out to determine the 5' terminal sequence using primers ADQ36713-ADQ36717
XX and ADQ36720, resulting in isolation of the 5' cDNA clones pBGDC 60
XX (ADQ36718), pBGDC 61 (ADQ36719), pGDC 63 (ADQ36721) and pGDC 64
XX (ADQ36722) and the full-length clones ADQ36723 and ADQ36724.
XX
XX Sequence 2045 BP; 402 A; 697 C; 598 G; 348 T; 0 U; 0 Other;
XX
XX Query Match 75.3%; Score 1611; DB 12; Length 2045;
XX Best Local Similarity 95.6%; Pred. No. 4.6e-257;

Matches 2044; Conservative 0; Mismatches 0; Indels 93; Gaps 34;
Qy 4 CTTTCTGCTGCTCCCTCTCTCCGTCATGAGACCGGCTGTGTCGCAAGCTATCG 63
Db 1 CTTTCTGCTGCTCCCTCTCTCCGTCATGAGACCGGCTGTGTCGCAAGCTATCG 60
Qy 64 TGGCGCGCCCGCTGGCGGCAAGCCCGGCTGCTCCGCGCGCTGAGCCGTGGGTCC 123
Db 61 TGGCC-----TGGCGGTGGTCC 78
Qy 124 GCTCCGCAAGCGGATGTCGGGCGCAAGGCGGCTTGTGAGGAGACATCCGCGA 183
Db 79 GCTCCGCAAGCGGATGTCGGGCGCAAGGCGGCTTGTGAGGAGACATCCGCGA 137
Qy 184 TGAAGCCACCAACCGGAGCTTCAAGCGGCTGAGAGAGCGGTGAACAGATGGCCCA 243
Db 138 TGAAGCCACCAACCGGAGCTTCAAGCGGCTGAGAGAGCGGTGAACAGATGGCCCA 196
Qy 244 AGCGGCGACTGAGAGGCTGTGTGACGCGCATCAAGAACCCGACGTGCGCAGCTGTA 303
Db 197 AGCGGCGACTGAGAGGCTGTGTGACGCGCATCAAGAACCCGACGTGCGCAGCTGTA 255
Qy 304 CCGAGATCTTCATGAAGAACCCGAGAGAGAGATTGATGAGGCGGTGGAGGTG 363
Db 256 CCGAGATCTTCATGAAGAACCCGAGAGAGAGATTGATGAGGCGGTGGAGGTG 314
Qy 364 CCGTCTCCCTGACAGCCCGTGTGAGAGAGCCCGAGCTGTGCTGCCATCTTCAAGCAGA 423
Db 315 CCGTCTCCCTGACAGCCCGTGTGAGAGAGCCCGAGCTGTGCTGCCATCTTCAAGCAGA 373
Qy 424 TCGTTGAGCTGAGCGCGGTATCATCTTCCGCGTGTCTGAGAGAGCGGCAAC 483
Db 374 TCGTTGAGCTGAGCGCGGTATCATCTTCCGCGTGTCTGAGAGAGCGGCAAC 432
Qy 484 TGCAGGTCAACCGGCGCTTCGGGTGAGTACTGTCGCGCATCGGCGCCCTCAAGGGCG 543
Db 433 TGCAGGTCAACCGGCGCTTCGGGTGAGTACTGTCGCGCATCGGCGCCCTCAAGGGCG 491
Qy 544 GCTGCGCTTCAACCCCTCCGTGAACCTGTCAATCAATGAAGTCTTCTTGAAGCAGA 603
Db 492 GCTGCGCTTCAACCCCTCCGTGAACCTGTCAATCAATGAAGTCTTCTTGAAGCAGA 550
Qy 604 TCTTCAAGAACAGCTTGAACCACTTCCCATGAGGCGGCGGCAAGGCGCTCGACTTCG 663
Db 551 TCTTCAAGAACAGCTTGAACCACTTCCCATGAGGCGGCGGCAAGGCGCTCGACTTCG 609
Qy 664 ACCCAAGGCGCAAGAGGAGCGGAGGTGATGCGCTTCTGCACTGCTTATGACGAGC 723
Db 610 ACCCAAGGCGCAAGAGGAGCGGAGGTGATGCGCTTCTGCACTGCTTATGACGAGC 668
Qy 724 TGCAGCGCCACATCAGCTTACGTGAGAGAGCTGCGCGCGGCGACATCGCGTGGCGCG 783
Db 669 TGCAGCGCCACATCAGCTTACGTGAGAGAGCTGCGCGCGGCGACATCGCGTGGCGCG 727
Qy 784 GCGAGATTGCTTACTTTTGGCCAGTACAGGCGCATACCAAGACTTACACCGGCGTGC 843
Db 728 GCGAGATTGCTTACTTTTGGCCAGTACAGGCGCATACACAGACTTACACCGGCGTGC 786
Qy 844 TGACCCGGAAGGCGCAGAGATATGCGGCTCCGAGATCCGCGCGGAGCCACCGGCTTACG 903
Db 787 TGACCCGGAAGGCGCAGAGATATGCGGCTCCGAGATCCGCGGAGCCACCGGCTTACG 845
Qy 904 GCGCGGTGCTGTTTGTGAGAAAGCTGTGAAGGCAAGGCGAGAGCTTCAAGGCGCAAGC 963
Db 846 GCGCGGTGCTGTTTGTGAGAAAGCTGTGAAGGCAAGGCGAGAGCTTCAAGGCGCAAGC 904
Qy 964 GCTGCTGTGTGTGCGCGGCGCAAGTGGCCAGTACTGCGGAGAGCTGTGTGAGA 1023
Db 905 GCTGCTGTGTGTGCGCGGCGCAAGTGGCCAGTACTGCGGAGAGCTGTGTGAGA 963
Qy 1024 AGGCGGCAATCGCTGCTGCTGCGGCTGCGGCTGCGGAGGCTGATGAGAGCCCAAGGCT 1083
Db 964 AGGCGGCAATCGCTGCTGCTGCGGCTGCGGCTGCGGAGGCTGATGAGAGCCCAAGGCT 1021

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1084 TCACGCGGAGCAGCTGACGGGGGTGACAGCATGAGAGAGAAACAAGCGCGCGCA 1143
1022 TCACGCGGAGCAGCTGACGGGGGTGACAGCATGAGAGAA--AAGAGCAACAGCGCGCGCA 1079
1144 TCTCCGAGTACAGAGCAGCAACCGCGGTATATGTGGCGCAGCGCGCAAGCCTTGGAGC 1203
1080 TCTCCGAGTACAGAGCAGCAACCGCGGTATATGTGGCGA--GCCGCAAGCCTTGGAGC 1137
1204 TGAAGTCCAGAGTGAATCGCTTCCCTGCGCACCAGAGAGAGATGATGAGCAGC 1263
1138 TGAAGTCCAGAGTGAATCGCTTCCCTGCGCACC--AACAGATTCATGAGCAGC 1195
1264 ACGCGGAGCTGTATCAAGCAGCGCTGCAAGTACGTGTGAGAGGGCGCGCAAGTGGCCT 1323
1196 ACGCGGAGCTGTATCAAGCAGCGCTGCAAGTACGTGT--AGGGCGCGCAAGTGGCCT 1253
1324 CCACCAAGAGAGGCGCATCCACAAGTACCAAGAGCGCGCATCTATCGCGCGCGCAAG 1383
1254 CCACCAAGAGAGGCGCATCCACAAGTACCAAGAGCGCGCAT--TCTACTGCGCGCGCAAG 1311
1384 CGGCGCAACGCGCGCGCGGTGAGCGGCTGAGATGACCAAGAGCGCGCATGAGCC 1443
1312 CGGCGCAACGCGCGCGCGGTGAGCGGCTGAGAT--CCAGAGAGCGCGCATGAGCC 1369
1444 TGAAGTCCAGAGTGAATCGCTTCCCTGCGCACCAGAGAGAGATGATGAGCAGC 1503
1370 TGAAGTCCAGAGTGAATCGCTTCCCTGCGCACC--TCTAGAGAGATGATGAGCAGC 1427
1504 ACTCCGCGCATGGGGCGGTGCGCGAGTACAAATGTGACCTGCGCGCGCGCAAGTGC 1563
1428 ACTCCGCGCATGGGGCGGTGCGCGAGTACAAATGTGACCT--CTGCGCGCGCGCAAGTGC 1485
1564 CGGCGTTCACCAAGTGTGCTGATGCGGTCAAGCGCGCGCTGTTTAACTGCGCGCAG 1623
1486 CGGCGTTCACCAAGTGTGCTGATGCGGTCAAGCGCGCG--GCTGTTTAACTGCGCGCAG 1543
1524 CCACCAAGAGAGGCGCATCCACAAGTACCAAGAGCGCGCATCTTCTTGG 1683
1544 CCACCAAGAGAGGCGCATCCACAAGTACCAAGAGCGCGCATCTTCTTGG 1601
1684 AAGCGGCGCTTCTTCCAGCGAGGCGCGTCAAGCTGCGCGTTCATTAACCTGATATG 1743
1602 AAGCGGCGCTTCTTCCAGCGAGGCGCGTCAAGCTGCGCG--TCTATTAACCTGATATG 1659
1744 GCGGCGCGCTGCAATTCACCGCGAGAGAGATGAGCGCATGATGATGAGCAGC 1803
1660 GCGGCGCGCTGCAATTCACCGCGAGAGAGATGAGCG--CTTGAATGATGAGCAGC 1717
1804 CTATTTTTCGCGAGCGCGCTCAACCGCGAGAGCTCTTCCCGAGCGCTTAAGCGCT 1863
1718 CTATTTTTCGCGAGCGCGCTCAACCGCGAGAG--CTTCCCGCGAGCGCTTAAGCGCT 1775
1864 GAGCGCGCGCGCATCTTCCAGCATGCGCTGCGTTTGAAGCGCGTCAAGTACCGCAG 1923
1776 GAGCGCGCGCGCATCTTCCAGCATGCGCTGCGTTTGA--CGCTTCAAGTACCGCAG 1833
1924 CTTGTTGAGAGCGTCAAGCTCAATTCCTTTTATGATGATGAGCGCGCGCTGCGCGC 1983
1834 CTTGTTGAGAGCGTCAAGCTCAATTCCTTTTATGATG--TGGCGCGCGCGCTGCGCGC 1891
1884 GAAATTTTCGCGAGCGTGAAGAGTGGGTTCTAGCTGAGTGAAGCGCGCATGAGT 2043
1892 GAAATTTTCGCGAGCGTGAAGAGTGGGTTCTAGCTGAGT--CGCGAGTGAAGCGT 1949
2044 GTGCGTGCCTTGCCTGCGTGCAGCGAGATGATGATGATGATGATGATGATGATGAT 2103
1950 GTGCGTGCCTTGCCTGCGTGCAGCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2007
2104 AAGAGAGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
2008 AAGAGAGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAA 2044

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RESULT 15
AD036712
ID AD036712 standard; cDNA; 1922 BP.
XX
XX AD036712;
AC
XX 23-SEP-2004 (first entry)
DT
XX
XX NADP-specific GDH related clone pBDC53, SEQ ID 7.
DE
XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
KW NADP-specific GDH; NADP-specific glutamate dehydrogenase; ss.
XX
XX Chlorella sorokiniana.
OS
XX US2004128710-A1.
PN
XX
XX 01-JUL-2004.
PD
XX
XX 24-JUL-2003; 2003US-00627886.
PF
XX
XX 01-MAY-1998; 98US-00070844.
PR
XX
XX (SCHMIDT R. R.
PA (MILLER P.
XX
XX Schmidt R, Miller P;
PI
XX
XX WPI; 2004-531134/51.
DR
XX
XX Increasing or decreasing nitrogen metabolism in plant cells, for plant
PT with increased yield and improved tolerance to ammonia toxicity and
PT osmotic stress, by transforming plant cell with nucleic acid having
PT glutamate dehydrogenase activity.
XX
XX
XX Example 2: SEQ ID NO 7; 36bp; English.
XX
XX The present invention relates to increasing or decreasing the nitrogen
CC metabolism in plant cells by transforming a plant cell with a
CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
CC (AD036709, AD036729), a beta subunit of NADP-specific GDH (AD036709,
CC AD036731), or their fragments, which exhibits GDH activity. The
CC polynucleotide is operably linked to a polynucleotide encoding a
CC chloroplast transit peptide comprising AD036710 or AD036711, or their
CC fragments that exhibit chloroplast transit activity. The method is useful
CC for increasing or decreasing the nitrogen metabolism in plant cells. The
CC methods, polynucleotides, and polypeptides are useful in producing plant
CC with increased yield, and with improved tolerance to ammonia toxicity,
CC osmotic stress, and composition of the crop or plant. The present
CC sequence is a cDNA clone which was isolated during the isolation of the
CC NADP-specific GDH cDNAs of the invention. Ten NADP-GDH clones were
CC identified in an example from the invention. Sequence analysis revealed
CC all ten clones were identical at their 3' termini and differed by varying
CC degree of truncation at their 5' termini. Clone pBDC53 (AD036712) was
CC the longest clone and was found to have a complete 3' terminus, but was
CC not long enough to encode either NADP-GDH subunit and so PCR was carried
CC out to determine the 5' terminal sequence using primers AD036713-AD036717
CC and AD036720, resulting in isolation of the 5' cDNA clones pBDC 60
CC (AD036718), pBDC 61 (AD036719), pBDC 63 (AD036721) and pBDC 64
CC (AD036722) and the full-length clones AD036723 and AD036724.
XX
XX Sequence 1922 BP; 393 A; 638 C; 567 G; 324 T; 0 U; 0 Other;
SQ

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Query Match 73.1%; Score 1565; DB 12; Length 1922;
Best Local Similarity 97.6%; Pred. No. 1.8e-249;
Matches 1922; Conservative 0; Mismatches 0; Indels 47; Gaps 31;

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171 CAGATCTCCGAGTGAAGCGCGCATCTTCAAGCGGTGAGAGAGCGGTGAG 230
1 CAGATCTCCGAGTGAAGCGCGCATCTTCAAGCGGTGAGAGAGCGGTGAG 60

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Qy 231 CAGATGGCCACCAAGGCGGCACTGAGGGCCCTGGTGCACGCGCATCAAGAACCCCGACGTG 290
Db 61 CAGATGGCCACCAAGGCGGCACTGAGGGCCCTGGTGCACGCGCATCAAGAACCCCGACGT- 119
Qy 291 CGCCAGCTGCTGACCGAGATCTTCAATGAAGAACCCGAGACGACGAGAGTTCATGACGGCG 350
Db 120 CGCCAGCTGCTGACCGAGATCTTCAATGAAGAACCCGAGACGACGAGAGTTCATGACGGCG- 178
Qy 351 GTGGCGGAGGTGGCGGTCTCCCTGACGCGGTGTTCCAGAAAGCCGCCGAGCTGTGCCC 410
Db 179 GTGGCGGAGGTGGCGGTCTCCCTGACGCGGTGTTCCAGAAAGCCGCCGAGCTGTG-CC 237
Qy 411 ATCTTCAAGCAGATGTTGAGCTGAGCGCGTGAATCACTTCCGCGTGTCTGTGCTGAGC 470
Db 238 ATCTTCAAGCAGATGTTGAGCTGAGCGCGTGAATCACTTCCGCGTGTCTGTGCTGAG- 296
Qy 471 GAGCGCGGCAACTGACAGTCAACCGCGGCTTCCGCGTGCAGTACTGTCGCCCATGGCG 530
Db 297 GAGCGCGGCAACTGACAGTCAACCGCGGCTTCCGCGTGCAGTACTGTCGCCCATGGCG- 355
Qy 531 CCCTAAGAGGCGCGCGCTTCCACCCCTCCGTAACCTGTCCATCATGTAAGTTCCCT 590
Db 356 CCCTAAGAGGCGCGCGCTTCCACCCCTCCGTAACCTGTCCATCATGTAAGTTCC- 414
Qy 591 GCCTTTGAGCAGATCTTCAAGAGAGCCTGACCACTCTGCCATGAGCGCGGCAAGGCG 650
Db 415 GCCTTTGAGCAGATCTTCAAGAGAGCCTGACCACTCTGCCATGAGCGCGGCGGCAAGGCG- 473
Qy 651 GGCCTCCGACTTTCGACCCCCAAGGCGAAGAGCGACGCGAGGTGATGCGCTTCTGCCAGTCC 710
Db 474 GGCCTCCGACTTTCGACCCCCAAGGCGAAGAGCGACGCGAGGTGATGCGCTTCTGCCAGT-C 532
Qy 711 TTCAATGACCGAGCTGACGCGCCACATCACTGACGAGAGCGTGCAGCGCGGCGGAGCATC 770
Db 533 TTCAATGACCGAGCTGACGCGCCACATCACTGACGAGAGCGTGCAGCGCGGCGGAGCAT- 591
Qy 771 GGCCTGAGCGCGCGCGAGATTGGCTACTCTTTCGCGCAGTACCAAGCGCATCCCAAGAC 830
Db 592 GGCCTGAGCGCGCGCGAGATTGGCTACTCTTTCGCGCAGTACCAAGCGCATCCCAAGAA- 650
Qy 831 TACACCGGCGTGTGACCCCGAAGGCGCAAGATGAGCGGCTCCGAGATCCGCCCGAG 890
Db 651 TACACCGGCGTGTGACCCCGAAGGCGCAAGATGAGCGGCTCCGAGATCCGCCCGAG- 709
Qy 891 GCCACCGGCTACGCGGCGCGTGTGTTGTGGAACCGTGAAGGACCAAGGCGAGAGCG 950
Db 710 GCCACCGGCTACGCGGCGCGTGTGTTGTGGAACCGTGAAGGACCAAGGCGAGAG- 768
Qy 951 CTCAAGGCGCAAGCGCTGCTGTGTGCGCGCGGCAACTGTGCGCCAGTACTGTGCGGAG 1010
Db 769 CTCAAGGCGCAAGCGCTGCTGTGTGCGCGCGGCAAGTGTGCGCCAGTACTGTGCGGAG- 827
Qy 1011 CTGCTGCTGAGAAAGGCGCGCATGTGTGTGCTGTGCTGCTCCAGCTCCAGGCGTACGTGTAC 1070
Db 828 CTGCTGCTGAGAAAGGCGCGCATGTGTGTGCTGTGCTGCTCCAGGCGTACGTGTAC- 886
Qy 1071 GAGCGCCAAAGCGCTTCAAGCGCGGAGAGCTGAGCGCGGTGCGAGCAATGAAAGAAAGAC 1130
Db 887 GAGCGCCAAAGCGCTTCAAGCGCGGAGAGCTGAGCGCGGTGCGAGCAATGAAAGAAAGAA- 945
Qy 1131 AACAGCGCGCGCATCTCCGATGACAGAGCAACCGCGGTGTATGTGTGAGGAGCGCGC 1190
Db 946 AACAGCGCGCGCATCTCCGATGACAGAGCAACCGCGGTGTATGTGTGAGGAGCGCGC--C 1003
Qy 1191 AAGCTTTGGAGCTGTGACTGCAAGTGAATCGCTTTCCCTGCGGCCACCCAGAACGAG 1250
Db 1004 AAGCTTTGGAGCTGTGACTGCAAGTGAATCGCTTTCCCTGCGGCCACCCAGAAC--G 1061
Qy 1251 ATCGATGAGCAAGAGCGCGAGCTGTATCAAGAGCGCGCTGCCAGTACGTGTGTGAGGCGC 1310
Db 1062 ATCGATGAGCAAGAGCGCGAGCTGTATCAAGAGCGCGCTGCCAGTACGTGTGTGAGGCG- 1119
Qy 1311 GCCAATGCGCTCCACCAAGAGGCGCATCCCAAGTACCAAGAGCGCGGCGATCATCTAC 1370

Db 1120 GCCAATGCGCTCCACCAAGAGGCGCATCCCAAGTACCAAGAGCGCGGCGATCATCT-- 1177
Qy 1371 TGCCCCCGGCAAGGCGGCGCAAGCGCGGCGGTGCGCGCTCAAGCGGCTTGAAGTACCCAG 1430
Db 1178 TGCCCCCGGCAAGGCGGCGCAAGCGCGGCGGTGCGCGCTTGAAGTACCC-- 1235
Qy 1431 AACCGATGAGCGCTGAAGTGAAGTTCGAGAGAGGTTGCGCAACAAAGCTGAGCGCATATG 1490
Db 1236 AACCGATGAGCGCTGAAGTGAAGTTCGAGAGAGGTTGCGCAACAAAGCTGAGCGCATAT- 1293
Qy 1491 AAGGACATCTACGACTCCGCGCATGAGGCGCTTCCCGCAGATACAAATGTTGACTGTGCG 1550
Db 1294 AAGGACATCTACGACTCCGCGCATGAGGCGCTTCCCGCAGATACAAATGTTGACTGTGCT- 1351
Qy 1551 GCGCGCAACATCGCGGCGCTTCAACAAAGTGTGATTCGCTCAAGGCGCGGCGGCTGTT 1610
Db 1352 GCGCGCAACATCGCGGCGCTTCAACAAAGTGTGATTCGCTCAAGGCGCGGCGGCTG- 1409
Qy 1611 TAACTGCGCGGCGCGCAAGGCGAGGCTCAACGCGCAATCCAAACCAACTCAACGCGC 1670
Db 1410 TAACTGCGCGGCGCGCAAGGCGAGGCTCAACGCGCAATCCAAACCAACTCAACGCG-- 1467
Qy 1671 AAGACCTTTTGGAGAGGCGGCGCTTTTCCAGCGAGGCGCTTCACTGTGCTTTCAATAA 1730
Db 1468 AAGACCTTTTGGAGAGGCGGCGCTTTTCCAGCGAGGCGCGCTTCACTGTGCTTTCAAT- 1525
Qy 1731 CCCCTGATTTGCGCGCGCTGCGCGCTGCAATTCACCCCGCAAGAACTAAGGCGCATGAC 1790
Db 1526 CCCCTGATTTGCGCGCGCTGCGCGCTGCAATTCACCCCGCAAGAACTAAGGCGCATG- 1583
Qy 1791 TGCAATCAGAGCGGCTATTTTGTGCGAGCGCGGCTCAACCCCGAGAGGCTCTCCCCCG 1850
Db 1584 TGCAATCAGAGCGGCTATTTTGTGCGAGCGCGGCTCAACCCCGAGAGGCTCTCCCC-- 1641
Qy 1851 AGCCCTAAGCGCTGACGCTCGCGCGCATTTGCTGTGCAATCGCTGCGTTTGAACCCCT 1910
Db 1642 AGCCCTAAGCGCTGACGCTCGCGCGCATTTGCTGTGCAATCGCTGCGTTTGAACCC-- 1699
Qy 1911 CCACTTACCCCAACCGCTGTGGAAGCCTTACAGCTCAATTGCTTTAAGTATGTGCGC 1970
Db 1700 CCACTTACCCCAACCGCTGTGGAAGCCTTACAGCTCAATTGCTTTAAGTATGT--GC 1757
Qy 1971 CCCCTCTGCGCGCGCAATTTTCTGCGCATGAGAGCTGCGGTTCTTACCTGTGACCCCA 2030
Db 1758 CCCCTCTGCGCGCGCAATTTTCTGCGCATGAGAGCTGCGGTTCTTACCTGTGACCC-- 1815
Qy 2031 AGTAGAGTTAGTGTGCTGCTGCTGCGCTGCGCTGCGCGGATGCGATTACTGTGACCTGA 2090
Db 1816 AGTAGAGTTAGTGTGCTGCTGCTGCGCTGCGCTGCGCGGATGCGATTACTGTGACCT-- 1873
Qy 2091 GAGTGTCTGTGTAAACGAGAGGCTCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 2139
Db 1874 GAGTGTCTGTGTAAACGAGAGGCTCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1922

Search completed: July 9, 2005, 19:27:18
Job time : 1088 secs

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OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 18:17:32 ; Search time 379 Seconds

(without alignments)
9239.135 Million cell updates/sec

Title: US-10-627-886-1
Perfect score: 2140
Sequence: 1 CTCCTTCTGCTGCGCCCTCT.....AAAAAAAAAAAAAAAAAAAA 2140

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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ALIGNMENTS

RESULT 1
US-08-541-033A-1
Sequence 1, Application US/08541033A
Patent No. 5879941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE ' AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33...1610
US-08-541-033A-1
Query Match 100.0%; Score 2140; DB 2; Length 2140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-828-451-1
: Sequence 1, Application US/08828451
: Patent No. 5985634
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: GENERAL INFORMATION:
: APPLICANT: Schmidt, Robert R.
: APPLICANT: Miller, Philip
: TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
: TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
: TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,451
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/541,033
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Whitlock, Ted W.
: REGISTRATION NUMBER: 36,965
: REFERENCE/DOCKET NUMBER: UP155
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (904) 375-8100
: TELEFAX: (904) 372-5800
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 33..1610
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: US-08-828-451-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-541-033A-18
Sequence 18, Application US/08541033A

Patent No. 5879941
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE - AND - SUBUNITS OF GLUTAMATE

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Saliwanichik & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida

COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-541-033A-18

Query Match 99.9%; Score 2137; DB 2; Length 2137;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 901 GCGCGCTGCTGTTTGTGAGAACTGTCTGAAGAACTGAAGGCGAGGCTTCAAGGCGAAGC 960
QY 964 GCTGCTGTGTCTGCGCGCGGCAACGTGCGCCAGTACTGCGCGGAGCTGTCTGAGAGA 1023
DB 961 GCTGCTGTGTCTGCGCGCGGCAACGTGCGCCAGTACTGCGCGGAGCTGTCTGAGAGA 1020
QY 1024 AGGGGCGCATGT 1083
DB 1021 AGGGGCGCATGT 1080
QY 1084 TCACGCGGAGCAGCTGACGAGCGGTGACAGACATGAAGAAAGAAACAACAGCGCGCA 1143
DB 1081 TCACGCGGAGCAGCTGACGAGCGGTGACAGACATGAAGAAAGAAACAACAGCGCGCA 1140
QY 1144 TCTCGAGTACAAAGAGCACAACCGCGGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGT 1203
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QY 1204 TGGACTGACAGTGAACATCGCTTCCCTGCGGCAACCAAGAAAGAACTGATGAGCAG 1263
DB 1201 TGGACTGACAGTGAACATCGCTTCCCTGCGGCAACCAAGAAAGAACTGATGAGCAG 1260
QY 1264 AGCGGAGCTGCTGATCAAGCAGCGCTGACAGTACGTGTGAGAGGCGCAACATGCGCT 1323
DB 1261 AGCGGAGCTGCTGATCAAGCAGCGCTGACAGTACGTGTGAGAGGCGCAACATGCGCT 1320
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QY 1384 CGGCGCAAGCGCGCGCGGTGCGGCGGTGACGCGCTGAGATGACCAAGAACCGCATGAGCC 1443
DB 1381 CGGCGCAAGCGCGCGCGGTGCGGCGGTGACGCGCTGAGATGACCAAGAACCGCATGAGCC 1440
QY 1444 TGAAGTGAAGCTGCGGAGAGGTTGCGGAGCTGAGGAGGATCAATGAAGGACATCTACG 1503
DB 1441 TGAAGTGAAGCTGCGGAGAGGTTGCGGAGCTGAGGAGGATCAATGAAGGACATCTACG 1500
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DB 1621 CCAGAGGAGGCTGACGCGGCAATCCAAAGGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1680
QY 1684 AAGCGGCGCTTTTCCAGCGAGGCGCTTCACTGCGCTTTCATTAACCTGTGATTTGCC 1743
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QY 1744 GCGGTGCGCTGCAATTCACCCCAAGAAAGAACTGAGCGGCACTGTGATGAGAGCGG 1803
DB 1741 GCGGTGCGCTGCAATTCACCCCAAGAAAGAACTGAGCGGCACTGTGATGAGAGCGG 1800
QY 1804 CTATTTTTTGGCGAGCGGCGGTACCCGAGAGGCTGTCTCCCGGAGCGCTTAAGCGCT 1863

DB 1801 CTATTTTTTGGCGAGCGGCGCTCACCCGAGAGCTCTCCCCGAGCGCTTAAGCGCT 1860
QY 1864 GACGTCCGCCGACTTTGCTCTGCAATCGCTCGGTTTGAACCCCTCAGTCTAACCAAC 1923
DB 1861 GACGTCCGCCGACTTTGCTCTGCAATCGCTCGGTTTGAACCCCTCAGTCTAACCAAC 1920
QY 1924 CCGTGTGAGAGCTTACAGTCAATGCGCTTATGATGATGAGCGCGCGCTCCGCGCCG 1983
DB 1921 CCGTGTGAGAGCTTACAGTCAATGCGCTTATGATGATGAGCGCGCGCTCCGCGCCG 1980
QY 1984 CGAATTTTCTGCGCATGAGAGCTGCGGTTCTTACCTGTGAGCCCAAGTAGCAGTTAGT 2043
DB 1981 CGAATTTTCTGCGCATGAGAGCTGCGGTTCTTACCTGTGAGCCCAAGTAGCAGTTAGT 2040
QY 2044 GTGCGTGTGCTGCGCTGCGCTGCGCGGAGTGCATGACTGAGCTGAGAGTCTTGTGTA 2103
DB 2041 GTGCGTGTGCTGCGCTGCGCTGCGCGGAGTGCATGACTGAGAGTCTGAGAGTCTTGTGTA 2100
QY 2104 AACACGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2140
DB 2101 AACACGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2137

RESULT 4
US-08-828-451-18
; Sequence 18, Application US/08828451
; Patent No. 5985634
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanhik & Saliwanhik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,451
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,033
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Whitlock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UFI155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-828-451-18

Query Match 99.9%; Score 2137; DB 2; Length 2137;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CTTTCTGCTCCGCTCTCTCCGATCCCGCATGACAGACCGGCTGTGCGCAAGGCTTACG 63
1 CTTTCTGCTCCGCTCTCTCTCCGATCCCGCATGACAGACCGGCTGTGCGCAAGGCTTACG 60
64 TGGCCGCGCCGCTGGCGGACGCGCGCGCTGTCGCGCGGTGGCGCGGTGGCTTC 123
61 TGGCCGCGCCGCTGGCGGACGCGCGCGCTGTCGCGCGGTGGCGCGGTGGCTTC 120
124 GCTCCGCGCAAGCGGATGTCGCGCGCAAGGCGGTGTCGCTGAGAGAGATCTCCGCGA 183
121 GCTCCGCGCAAGCGGATGTCGCGCGCAAGGCGGTGTCGCTGAGAGAGATCTCCGCGA 180
184 TGAAGCGCACCAACCGGCGACTTTCACGCGCGCTGACAGAAAGCGGTGAAGAGATGCGCA 243
181 TGAAGCGCACCAACCGGCGACTTTCACGCGCGCTGACAGAAAGCGGTGAAGAGATGCGCA 240
244 AGCGCGGAGCATGAGGCGCTGTGTGCACGGCATCAAGAAACCCGACGCTGCGCATGCTGA 303
241 AGCGCGGAGCATGAGGCGCTGTGTGCACGGCATCAAGAAACCCGACGCTGCTGA 300
304 CCGAGATCTTATGAAAGAACCGGAGACGAGAGATTATGACAGCGGTGGCGAGGTGG 363
301 CCGAGATCTTATGAAAGAACCGGAGACGAGAGATTATGACAGCGGTGGCGAGGTGG 360
364 CCGTCTCCCTGACGCGCGTGTTCGAGAAAGCGCCCGAGCTGTGCCATCTTTCAGACGAG 423
361 CCGTCTCCCTGACGCGCGTGTTCGAGAAAGCGCCCGAGCTGTGCCATCTTTCAGACGAG 420
424 TCGTTGAGCTTGAGCGCGTATCACTTTCGCGGTGTCTGTGCTGAGACGCGCGCAAC 483
421 TCGTTGAGCTTGAGCGCGTATCACTTTCGCGGTGTCTGTGCTGAGACGCGCGCAAC 480
484 TGAAGGTCAACCGGCGCTTCCGCGTGCAGTACTGTCGCGCATGCGCCCTTACAAAGGCG 543
481 TGAAGGTCAACCGGCGCTTCCGCGTGCAGTACTGTCGCGCATGCGCCCTTACAAAGGCG 540
544 GCGTGGCTTCAACCCCTCCGCTGAACCTGTCCATCATGAATTCCTTTCAGTGAAGCAGA 603
541 GCGTGGCTTCAACCCCTCCGCTGAACCTGTCCATCATGAATTCCTTTCAGTGAAGCAGA 600
604 TCTTCAAGAACGCTTGAACCAACCTGCGCATGAGCGCGCGCAAGGCGGCTTCCGACTTTCG 663
601 TCTTCAAGAACGCTTGAACCAACCTGCGCATGAGCGCGCGCAAGGCGGCTTCCGACTTTCG 660
664 ACCCAAGGAGGAGGAGCGCGAGGTGATGCGCTTTCGACGTCCTTCAATGACCGAGC 723
661 ACCCAAGGAGGAGGAGCGCGAGGTGATGCGCTTTCGACGTCCTTCAATGACCGAGC 720
724 TGAAGCGCACATGAGTACGTGACGAGAGCTGCCCGCGGACATCGGCGTGGCGCGC 783
721 TGAAGCGCACATGAGTACGTGACGAGAGCTGCCCGCGGACATCGGCGTGGCGCGC 780
784 GCGAGATGAGTACCTTTTGGGCGAGTACAAAGCGCATCAACCAAGAACTTACACCGGCTGC 843
781 GCGAGATGAGTACCTTTTGGGCGAGTACAAAGCGCATCAACCAAGAACTTACACCGGCTGC 840
844 TGAAGCGGAGGAGGAGGAGTATGCGCGGCTCCGAGATCCGCGGACCAACCGGCTTACG 903
841 TGAAGCGGAGGAGGAGGAGTATGCGCGGCTCCGAGATCCGCGGACCAACCGGCTTACG 900
904 GCGCGTGTCTTTTGTGAGAAAGTGAAGAGCAAGGAGGAGGAGCTTCAAGGAGCAAGC 963
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964 GCTGCTGTGTCTTGGCGGAGCAAGTGGCCAGTACTGCGCGAGAGTGTGCTGAGAG 1023
961 GCTGCTGTGTCTTGGCGGAGCAAGTGGCCAGTACTGCGCGAGAGTGTGCTGAGAG 1020
1024 AGGCGCGCATGCTGTGTGCTGCTGCTGCGCATGCGGAGGAGTATGAGTACAGGCGCAACG 1083
1021 AGGCGCGCATGCTGTGTGCTGCTGCTGCGCATGCGGAGGAGTATGAGTACAGGCGCAACG 1080

1084 TCAAGCGGAGGAGCTTCAGGCGGTGCGAGGACATGAAAGAAAGAACAGCGCCCGCA 1143
1081 TCAAGCGGAGGAGCTTCAGGCGGTGCGAGGACATGAAAGAAAGAACAGCGCCCGCA 1140
1144 TCTCCGAGTACAAAGAGGAGACCGCGCTGTATGTGGCGACCCGCGCAAGCTTGGAGC 1203
1141 TCTCCGAGTACAAAGAGGAGACCGCGCTGTATGTGGCGACCCGCGCAAGCTTGGAGC 1200
1204 TGAAGTGCAGGTTGAGCATGCGCTTCCCTGCGGACCCAGAAAGGAGATGATGAGCAGC 1263
1201 TGAAGTGCAGGTTGAGCATGCGCTTCCCTGCGGACCCAGAAAGGAGATGATGAGCAGC 1260
1264 AGCGGAGCTGTGATCAAGACGCGCTGCCAGTACGTGTGAGAGGCGCAATGCGCTT 1323
1261 AGCGGAGCTGTGATCAAGACGCGCTGCCAGTACGTGTGAGAGGCGCAATGCGCTT 1320
1324 CCACCAAGAGGCGCATCAAGATGATCAAGAGGCGCGCATCTTATCTGCGCGGCAAG 1383
1321 CCACCAAGAGGCGCATCAAGATGATCAAGAGGCGCGCATCTTATCTGCGCGGCAAG 1380
1384 CGGCGCAAGCGCGGCGGTGGCGGTGACGCGGCTGAGATGACCCAGAACCGCATGAGCC 1443
1381 CGGCGCAAGCGCGGCGGTGGCGGTGACGCGGCTGAGATGACCCAGAACCGCATGAGCC 1440
1444 TGAAGTGAATCTGCGAGAGGATTCGCGACAAAGCTGAGCGCATCATGAAAGACATCTACG 1503
1441 TGAAGTGAATCTGCGAGAGGATTCGCGACAAAGCTGAGCGCATCATGAAAGACATCTACG 1500
1504 ACTCCGCGATGGGCGGTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1563
1501 ACTCCGCGATGGGCGGTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1564 CGGCGTTCACCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
1561 CGGCGTTCACCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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1621 CCCAAGCACGCGCTCACCGGCAATCCAAACCAACCAACCAACCAACCAACCAACCAAC 1680
1684 AAGCGGCGCTTTTTCAGGCGGAGGCGCTTCACTGCGCTTTCATTAACCTTGTGATTTGGC 1743
1681 AAGCGGCGCTTTTTCAGGCGGAGGCGCTTCACTGCGCTTTCATTAACCTTGTGATTTGGC 1740
1744 GCGGTGCGCTTGAATTCACACCCCAAGAAAGCTTGAAGGAGCACTTGAATGAGAGCAG 1803
1741 GCGGTGCGCTTGAATTCACACCCCAAGAAAGCTTGAAGGAGCACTTGAATGAGAGCAG 1800
1804 CTATTTTTTTCGCGAGCGGCGCTTCAACCCGAGAGCTTCTTCCCGAGCGCTTAAAGCGCT 1863
1801 CTATTTTTTTCGCGAGCGGCGCTTCAACCCGAGAGCTTCTTCCCGAGCGCTTAAAGCGCT 1860
1864 GAGGTCCGCGGAGCTTTTGGCTTGGCAATGCTGGTGTGATGATGATGATGATGATGATGAT 1923
1861 GAGGTCCGCGGAGCTTTTGGCTTGGCAATGCTGGTGTGATGATGATGATGATGATGATGAT 1920
1924 CCGTGTGAGAGCTTACAGTCAATGCTTGAATGATGATGATGATGATGATGATGATGATGAT 1983
1921 CCGTGTGAGAGCTTACAGTCAATGCTTGAATGATGATGATGATGATGATGATGATGATGAT 1980
1984 GAAATTTTTCGCGCATGAGAGCTGCGGTTCTTACGCTGATGACCCCAAGATGAGTATGAT 2043
1981 GAAATTTTTCGCGCATGAGAGCTGCGGTTCTTACGCTGATGACCCCAAGATGAGTATGAT 2040
2044 GTGCGTGTGCTTGGCTTGGCTGCGCGGAGATGAGTATGATGATGATGATGATGATGATGAT 2103
2041 GTGCGTGTGCTTGGCTTGGCTGCGCGGAGATGAGTATGATGATGATGATGATGATGATGAT 2100
2104 AACACGAGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
2101 AACACGAGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2137

Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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Qy 4 CTTTCTGTCGACCTCTCTCCGTCCCGCATGACAGACCGCCCTGTCGCAAGGCTATCG 63
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Qy 64 TGCGCGCCCGCTGAGCGGACGCGCGCTGCTCGCGCGGTGACCGCTGCGGTGCTC 123
Db 61 TGCGC-----TGCGCGTGGGTCC 78
Qy 124 GCTCCGCGCAAGCGGATGTCGCGCGCAAGGCGCTGTCGCTGGAGAGAGATGTCGCGGA 183
Db 79 GCTCCGCGCAAGCGGATGTCGCGCGCAAGGCGCTGTCGCTGGAGAGAGATGTCGCGGA 138
Qy 184 TGAAGCGCACCAACCGGCACTTCAACGCGCTGCAAGAAAGCGGTGAAGAGATGCGCACCA 243
Db 139 TGAAGCGCACCAACCGGCACTTCAACGCGCTGCAAGAAAGCGGTGAAGAGATGCGCACCA 198
Qy 244 AGCGGGGCACTGAGGGGCTGATGCAACGCGATCAAGAAACCCGACGCTGCGCATGCTGA 303
Db 199 AGCGGGGCACTGAGGGGCTGATGCAACGCGATCAAGAAACCCGACGCTGCTGA 258
Qy 304 CCGAGATCTTCAATGAAGAACCCGAGACGACGAGATTCATGCAAGCGGTGCGGAGGTGG 363
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Qy 364 CCGATCTCCCTGACGCGCGTGTTCGAGAAAGCGCCCGAGCTGTCGCCCATCTTCAAGCAGA 423
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Qy 424 TCGTTGAGCCTGAGCGCGTGAATCACTTCGCGGTGCTGAGTCGACGCGCGCAAC 483
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Qy 484 TGCAGGTCAACCGGCGCTTCGCGGTGCACTGTCGCGCATGAGGCCCTTCAAGAGGCG 543
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Db 499 GCGTCGCTTCAACCCCTCCGTGAAACCTGTCATCATGAATTCCTTGGAGAGAGA 558
Qy 604 TCTTCAAGAACGCTGACACCCCTGCGCATGGCGGCGGCAAGGCGGCTCCGACTTCG 663
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Db 619 ACCCAAGGGGCAAGAGCGCGAGGTGATGCGCTTTCGCAATGCTTCAATGACCAAGC 678
Qy 724 TGCAGCGCACATGACTAGTGAAGAGAGTCCCGCGCGACATCGCGCTGGCGCGC 783
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Db 799 TGAACCCGGAAGGGCAGAGATGAGCGGCTCCGAGATCCGCGCGACCGGCTTACG 858
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Qy 1384 CCGCAAGCGCGGCGGTGCGGCTGACGCGGCTGAGATGACCCAGAACCGCATGAGCC 1443
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Db 1999 GTGCTGCTTTGCGCTGCGCTGCGCGGAGTGCATCTGTGACTGAGAGTCTTGTGTA 2058
Qy 2104 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db 2059 AACAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2095
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1444 TGAAGTGAAGTGGAGAGGTTGCGACAGTGAAGCGCATGAGAGCATCTACG 1503
1399 TGAAGTGAAGTGGAGAGGTTGCGACAGTGAAGCGCATGAGAGCATCTACG 1458
1504 ACTCGGCAATGAGGCGCTCCCGCAGATCAATGTTGACTGCGGCGCCCAATCG 1563
1459 ACTCGGCAATGAGGCGCTCCCGCAGATCAATGTTGACTGCGGCGCCCAATCG 1518
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1699 GCGGTCGCGCTGCAATTCACCCCAAGAGAACTAGGCGCACTGATGATGAGAGCG 1758
1804 CTATTTTTCGCGACGCGCTCAACCCGAGAGCTCTCTCCCGAGCGCTTAAGCGCT 1863
1759 CTATTTTTCGCGACGCGCTCAACCCGAGAGCTCTCTCCCGAGCGCTTAAGCGCT 1818
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1819 GACGTCGCGCGAGCTTGGCTGCGACATGCTGCGTTTGAACCCCTCTCACTCAAC 1878
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1879 CCGTGTGGAAGCTTACAGCTCAATGCTTGTAGTATGAGGCGCGCTCTGCGCC 1938
1984 CGAATTTTCTGCGATGAGAGCTGCTGCTTCTAGCTGATGAGCGCGAGTGAAGT 2043
1939 CGAATTTTCTGCGATGAGAGCTGCTGCTTCTAGCTGATGAGCGCGAGTGAAGT 1998
2044 GTGCGTCTGCTGCGCTGCGCTGCGCGAGATGAGTACTGATGAGAGTCTTGTGA 2103
1999 GTGCGTCTGCTGCGCTGCGCTGCGCGAGATGAGTACTGATGAGAGTCTTGTGA 2058
2104 AACGAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
2059 AACGAGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2095

RESULT 9
US-08-541-033A-7
Sequence 7, Application US/08541033A
Patent No. 5879941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanhik & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541, 033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-541-033A-7

Query Match 92.0%; Score 1969; DB 2; Length 1969;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CAGATCTCGCGATGAGAGCGCCACACCGGCACTTCAACGCGCTGCAAGAGCGGTGAAG 60
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61 CAGATGCGCCAAAGGCGGCACTGAGAGGCTGTGTGCAACGCGCATCAAGAACCCCGAGCTG 120
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181 GTGCGGAGGTGGCGGCTCTCTGCGAGCCGCTGTGCAAGAGCGCCCGAGCTGTGCCC 240
411 ATCTTCAAGCAGATCTTGAAGCTGAGCGGCTGATCACTTCCGCGTGTCTGCTGAGAC 470
241 ATCTTCAAGCAGATCTTGAAGCTGAGCGGCTGATCACTTCCGCGTGTCTGCTGAGAC 300
471 GAGCGCGGCAACCTGAGGTCAACCGCGGCTTCCGCGTGAATCTGTCGCGCATGCGC 530
301 GAGCGCGGCAACCTGAGGTCAACCGCGGCTTCCGCGTGAATCTGTCGCGCATGCGC 360
531 CCTTAAAGGCGGCGCTGCGCTTCAACCCCTCGTGAACCTGTTCATGATGAAGTCTT 590
361 CCTTAAAGGCGGCGCTGCGCTTCAACCCCTCGTGAACCTGTTCATGATGAAGTCTT 420
591 GCTTTGAGCAGATCTTCAAGAAAGAGCTTCAACCCCTCGTGAACCTGTTCATGATGAAG 650
421 GCTTTGAGCAGATCTTCAAGAAAGAGCTTCAACCCCTCGTGAACCTGTTCATGATGAAG 480
651 GCTTCCAGCTTCAACCCCAAGGCGCAAGAGCGGAGGTGATGCGCTTCTGCGAGTCC 710
481 GCTTCCAGCTTCAACCCCAAGGCGCAAGAGCGGAGGTGATGCGCTTCTGCGAGTCC 540
711 TTATGACCGAGCTGACGCGCCATCATGCTAGTGAAGAGTGTGCGCGCGAGATC 770
541 TTATGACCGAGCTGACGCGCCATCATGCTAGTGAAGAGTGTGCGCGCGAGATC 600
771 GCGTGGGCGCGCGAGATTTGCTACTTTTGGCGCAATGAAAGGCGCATCAAGAAAC 830
601 GCGTGGGCGCGCGAGATTTGCTACTTTTGGCGCAATGAAAGGCGCATCAAGAAAC 660
831 TACACCGGCGTGTGACCCCGAAGGCGCAGAGATGAGCGCTCCGAGATCCCGCGAG 890
661 TACACCGGCGTGTGACCCCGAAGGCGCAGAGATGAGCGCTCCGAGATCCCGCGAG 720
891 GCCACCGGCTTACGCGCGCGTGTGTTGTGAGAAAGTGTGAGAGCAAGGCGAGAGC 950

QY 351 GTGCGAGAGTGGCGTCTCCCTGACGCGGTGTTGAGAAAGCGCCCGAGCTGTGCCC 410
Db 181 GTGCGAGAGTGGCGTCTCCCTGACGCGGTGTTGAGAAAGCGCCCGAGCTGTGCCC 240
QY 411 ATCTTCAAGCAGATCGTTGAGAGCTGAGGCTGATCACTTCCCGGTGTCTGTGCTGAC 470
Db 241 ATCTTCAAGCAGATCGTTGAGAGCTGAGGCTGATCACTTCCCGGTGTCTGTGCTGAC 300
QY 471 GAGCGCGGCAACCTGAGAGTCAACCGCGGCTTCCGCGTGAAGTCTGTCCGCGCATCGGC 530
Db 301 GAGCGCGGCAACCTGAGAGTCAACCGCGGCTTCCGCGTGAAGTCTGTCCGCGCATCGGC 360
QY 531 CCCTACAAAGGCGGCGCTGCGCTTCAACCCCTCGTGAACCTGTGCATCATGAAGTTCCTT 590
Db 361 CCCTACAAAGGCGGCGCTGCGCTTCAACCCCTCGTGAACCTGTGCATCATGAAGTTCCTT 420
QY 591 GCTTTGAGCAGATCTTCAAGAACAGCTGACACCTGTGCGGCAATGGGCGGCGGAAGGCG 650
Db 421 GCTTTGAGCAGATCTTCAAGAACAGCTGACACCTGTGCGGCAATGGGCGGCGGAAGGCG 480
QY 651 GGTCCGACTTCAACCCCAAGGAGAGCGAGCGGAGTGTGCGCTTCTGCGAGTCC 710
Db 481 GGTCCGACTTCAACCCCAAGGAGAGCGAGCGGAGTGTGCGCTTCTGCGAGTCC 540
QY 711 TTCAATGACGAGCTGACGCGGCAATCACTAGCTGACGAGCGTGCAGCGGCGGAGCATC 770
Db 541 TTCAATGACGAGCTGACGCGGCAATCACTAGCTGACGAGCGTGCAGCGGCGGAGCATC 600
QY 771 GGGCTGGGCGGCGGAGATTTGGCTACTTTTGGCGGCAATCAAGCGCATCAACCAAGAC 830
Db 601 GGGCTGGGCGGCGGAGATTTGGCTACTTTTGGCGGCAATCAAGCGCATCAACCAAGAC 660
QY 831 TACACCGGCGTGTGACCCCGGAAGGAGAGTATGAGCGGCTCGAGATCCGCGCGGAG 890
Db 661 TACACCGGCGTGTGACCCCGGAAGGAGAGTATGAGCGGCTCGAGATCCGCGCGGAG 720
QY 891 GCGACCGGCTACCGCGCGGT 950
Db 721 GCGACCGGCTACCGCGCGGT 780
QY 951 CTCAAGGAGGAGCGCTGT 1010
Db 781 CTCAAGGAGGAGCGCTGT 840
QY 1011 CTGTGCTGTGAGAGAGGAGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1070
Db 841 CTGTGCTGTGAGAGAGGAGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 1071 GAGCGCAACGCGCTTCAACCGCGGAGAGCTGTGAGGCGGTGACAGATGTAAAGAAAGAAC 1130
Db 901 GAGCGCAACGCGCTTCAACCGCGGAGAGCTGTGAGGCGGTGACAGATGTAAAGAAAGAAC 960
QY 1131 AACGAGCGCGCGCATCTCCGATCAAGAGCGACACCGCGGTGTGTGTGTGTGTGTGTGTGT 1190
Db 961 AACGAGCGCGCGCATCTCCGATCAAGAGCGACACCGCGGTGTGTGTGTGTGTGTGTGT 1020
QY 1191 AAGCGTTGGAGAGTGTGATGCGAGGTGAGATGTGCTTCCCTGTGCGGACACCGAGAG 1250
Db 1021 AAGCGTTGGAGAGTGTGATGCGAGGTGAGATGTGCTTCCCTGTGCGGACACCGAGAG 1080
QY 1251 ATCGATGAGCAGACGCGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1310
Db 1081 ATCGATGAGCAGACGCGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1311 GCGCAATGCGCTTCAACCAAGAGGCGCATCAAGAGTCAACCAAGGCGGCGGATCTTAC 1370
Db 1141 GCGCAATGCGCTTCAACCAAGAGGCGCATCAAGAGTCAACCAAGGCGGCGGATCTTAC 1200
QY 1371 TGCGCGGAGAGGCGGCGCAACGCGGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1430
Db 1201 TGCGCGGAGAGGCGGCGCAACGCGGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1431 AACCGCATGAGCTGTAACTGTGACTGTGAGAGAGTTTCCGCAACAGCTGTGAGCGCATATG 1490

Db 1261 AACCGCATGAGCTGTAACTGTGACTGTGAGAGAGTTTCCGCAACAGCTGTGAGCGCATATG 1320
QY 1491 AAGGACATTCACGACTCCGCGCATGGGCGGTCCCGAGATACATGTGACTGTGCGG 1550
Db 1321 AAGGACATTCACGACTCCGCGCATGGGCGGTCCCGAGATACATGTGACTGTGCGG 1380
QY 1551 GGGCGCAACATCGCGGCGCTTCAACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1610
Db 1381 GGGCGCAACATCGCGGCGCTTCAACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 1611 TAACTGCGGAGCGGCGCAACGAGCTGACCGGCAATCAACCAACCACTCAAGGCGC 1670
Db 1441 TAACTGCGGAGCGGCGCAACGAGCTGACCGGCAATCAACCAACCACTCAAGGCGC 1500
QY 1671 AAGACCTTTTGGAGAGGCGGCGCTTTTCCAGAGAGGCGCTCACTGCGCTTTCATTA 1730
Db 1501 AAGACCTTTTGGAGAGGCGGCGCTTTTCCAGAGAGGCGCTCACTGCGCTTTCATTA 1560
QY 1731 CCTGTATTTGCGGCGCGCTGTGCAATTCACCCCAAGAAAGAACTAGCGGCACTTGAC 1790
Db 1561 CCTGTATTTGCGGCGCGCTGTGCAATTCACCCCAAGAAAGAACTAGCGGCACTTGAC 1620
QY 1791 TGCAATGAGAGCGCTATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1850
Db 1621 TGCAATGAGAGCGCTATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 1851 AGGCGTAAAGGCGTGAAGTCCGCGGAGCTTGTGCTGTGAGCATGTGTGTGTGTGTGT 1910
Db 1681 AGGCGTAAAGGCGTGAAGTCCGCGGAGCTTGTGCTGTGAGCATGTGTGTGTGTGTGT 1740
QY 1911 CCACTACACCACTGT 1970
Db 1741 CCACTACACCACTGT 1800
QY 1971 CCGCTCTGCGGCGGAAATTTTCTGTGCAATGAGAGTGTGTGTGTGTGTGTGTGTGT 2030
Db 1801 CCGCTCTGCGGCGGAAATTTTCTGTGCAATGAGAGTGTGTGTGTGTGTGTGTGTGT 1860
QY 2031 AGTAGCATTAGT 2090
Db 1861 AGTAGCATTAGT 1920
QY 2091 GAGTGTGTGTGTAAACGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2139
Db 1921 GAGTGTGTGTGTAAACGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 1969

RESULT 11
US-08-541-033A-23
Sequence 23, Application US/08541033A
Patent No. 5879941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541, 033A

COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1506 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1464
US-08-828-451-23

Query Match 70.2%; Score 1501.4; DB 2; Length 1506;
Best Local Similarity 99.9%; Pred. No. 1.8e-295;
Matches 1502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 150 AAGCCGCTGCTGCTGAGAGACAGATCTCCGCGATGAGCCACCAACCGCGGACTTTCAG 209
DB 4 ATGGCCGCTGCTGCTGAGAGACAGATCTCCGCGATGAGCCACCAACCGCGGACTTTCAG 63
QY 210 GCGCTGCAGAAAGCGGCTGAGCAAGATGCGCACCAAGCGGCGACTGAGAGGCTTGATGAC 269
DB 64 GCGCTGCAGAAAGCGGCTGAGCAAGATGCGCACCAAGCGGCGACTGAGAGGCTTGATGAC 123
QY 270 GGCAATCAAGAACCCCGAGCTGCGCAGCTGCGACCGAGATCTTCATGAGAGAACCCCGAG 329
DB 124 GGCAATCAAGAACCCCGAGCTGCGCAGCTGCGACCGAGATCTTCATGAGAGAACCCCGAG 183
QY 330 CAGCAGAGATTTCATGAGAGCGGCTGCGAGGCTGCGCTCTCCCTGACAGCCGCTTTCAG 389
DB 184 CAGCAGAGATTTCATGAGAGCGGCTGCGAGGCTGCGCTCTCCCTGACAGCCGCTTTCAG 243
QY 390 AAGCGCCCGAGCTGCTGCCATCTTCAAGCAGATGTTGAGCTGAGCGCTGATAC 449
DB 244 AAGCGCCCGAGCTGCTGCCATCTTCAAGCAGATGTTGAGCTGAGCGCTGATAC 303
QY 450 TTCCGCGCTGCTGCTGAGAGAGCGCCGGAACCTGACAGTTCACCCGCGCTTTCAG 509
DB 304 TTCCGCGCTGCTGCTGAGAGAGCGCCGGAACCTGACAGTTCACCCGCGCTTTCAG 363
QY 510 CAGTACTGTCGCGCATCGGCCCTTCAAGAGGCGGCGCTGCGCTTTCACCCCTCGGTGAC 569
DB 364 CAGTACTGTCGCGCATCGGCCCTTCAAGAGGCGGCGCTGCGCTTTCACCCCTCGGTGAC 423
QY 570 CTGTCCATCATGAAGTCTTTCCTTTGAGCAGATCTTCAAGAACAGCTGATACCACTTG 629
DB 424 CTGTCCATCATGAAGTCTTTCCTTTGAGCAGATCTTCAAGAACAGCTGATACCACTTG 483
QY 630 CCCATGGGCGGCGGAGAGGCGGCTCCGACTTTCAGACCCCAAGGCGCAAGAGGAGAG 689
DB 484 CCCATGGGCGGCGGAGAGGCGGCTCCGACTTTCAGACCCCAAGGCGCAAGAGGAGAG 543

QY 690 GTGATGCGCTTTCGCGAGTCTTCATGACCGAGCTGAGCGGCAATCAGCTACGTGAG 749
DB 544 GTGATGCGCTTTCGCGAGTCTTCATGACCGAGCTGAGCGGCAATCAGCTACGTGAG 603
QY 750 GACGTGCGGCGGCGGAGCATCGGCGTGTGGGCGCGGAGATTGGCTACCTTTTCGGCAG 809
DB 604 GACGTGCGGCGGCGGAGCATCGGCGTGTGGGCGCGGAGATTGGCTACCTTTTCGGCAG 663
QY 810 TACAAGGCGATCAACCAAGACTACACCGGCGTGTGACCCCGAAGGCGCAGAGTATGCG 869
DB 664 TACAAGGCGATCAACCAAGACTACACCGGCGTGTGACCCCGAAGGCGCAGAGTATGCG 723
QY 870 GCGTCCGAGATCCGCGCGAGGCGCACCGGCTTACCGGCGCTGTTTGTGAGAACGTG 929
DB 724 GCGTCCGAGATCCGCGCGAGGCGCACCGGCTTACCGGCGCTGTTTGTGAGAACGTG 783
QY 930 CTGAAGGACAAAGGCGGAGACCTTCAAGGCGAACCGCTGCTGTGTGTGGCGGCGAAC 989
DB 784 CTGAAGGACAAAGGCGGAGACCTTCAAGGCGAACCGCTGCTGTGTGTGGCGGCGAAC 843
QY 990 GTGGCCCACTACTGCGCGAGCTGCTGTGAGAGAGGCGGCGCATCGTGTGCTGTCC 1049
DB 844 GTGGCCCACTACTGCGCGAGCTGCTGTGAGAGAGGCGGCGCATCGTGTGCTGTCC 903
QY 1050 GACTCCAGGCGCTACGTGTACGAGCCCAACGCGCTTCAACGCGAGCAGCTGACGCGGTG 1109
DB 904 GACTCCAGGCGCTACGTGTACGAGCCCAACGCGCTTCAACGCGAGCAGCTGACGCGGTG 963
QY 1110 CAGGACATGAAGAAAGAAACACAGGCGCGCATCTCCGAGTTCAGAGAGCGACACCGCC 1169
DB 964 CAGGACATGAAGAAAGAAACACAGGCGCGCATCTCCGAGTTCAGAGAGCGACACCGCC 1023
QY 1170 GTGTATGTGGGCGACCGCGCAAGCTTGGAGCTGAGCTGCCAGGTGACATCGCTTC 1229
DB 1024 GTGTATGTGGGCGACCGCGCAAGCTTGGAGCTGAGCTGCCAGGTGACATCGCTTC 1083
QY 1230 CCTGCGCCACCGAGAACGAGATGATGAGCAGCGCGAGCTGTGATCAAGCAGCGC 1289
DB 1084 CCTGCGCCACCGAGAACGAGATGATGAGCAGCGCGAGCTGTGATCAAGCAGCGC 1143
QY 1290 TGCCAGTACGTGTGTGAGAGGCGGCGCAATGCTCTCCACCAAGGCGCATCCCAAGTAC 1349
DB 1144 TGCCAGTACGTGTGTGAGAGGCGGCGCAATGCTCTCCACCAAGGCGCATCCCAAGTAC 1203
QY 1350 AACCAAGCGCGCATCATCTACTGCGCGGCAAGCGGCGCAAGCGCGCGCTGCGCGTC 1409
DB 1204 AACCAAGCGCGCATCATCTACTGCGCGGCAAGCGGCGCAAGCGCGCGCTGCGCGTC 1263
QY 1410 AGCGGCTGAGATGACCCCAAGAACCGCATGAGCTGAACTGGAATCGCGAGAGTTGCG 1469
DB 1264 AGCGGCTGAGATGACCCCAAGAACCGCATGAGCTGAACTGGAATCGCGAGAGTTGCG 1323
QY 1470 GACAACTGAGAGGCGCATCAAGAAAGCATCTTAAGACTCCCGCATTTGGGCGCTCCCGAGA 1529
DB 1324 GACAACTGAGAGGCGCATCAAGAAAGCATCTTAAGACTCCCGCATTTGGGCGCTCCCGAGA 1283
QY 1530 TACAATGTTAACCTGGCTGCGGCGGCGCAATGCGCGGCTTTCACCAAGTGTGCTGATGCC 1589
DB 1384 TACAATGTTAACCTGGCTGCGGCGGCGCAATGCGCGGCTTTCACCAAGTGTGCTGATGCC 1443
QY 1590 GTCAAGGCCCAAGGCGCTGTTTAAAGCTGCCAGAGCCCAAGCCACCGGCTCACCGGCAATCC 1649
DB 1444 GTCAAGGCCCAAGGCGCTGTTTAAAGCTGCCAGAGCCCAAGCCACCGGCTCACCGGCAATCC 1503
QY 1650 AAC 1652
DB 1504 AAC 1506

RESULT 13
US-08-541-033A-25
; Sequence 25, Application US/08541033A
; Patent No. 5879941

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 1st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1431
US-08-541-033A-25

Query Match 68.7%; Score 1470; DB 2; Length 1473;
Best Local Similarity 100.0%; Pred. No. 4.1e-289;
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 ATGACGCGCACCGGCGGACCTTCAAGCGCGTGCAGAGCGGTGAAGCAAGTGGCCACC 242
DB 4 ATGACGCGCACCGGCGGACCTTCAAGCGCGTGCAGAGCGGTGAAGCAAGTGGCCACC 63
QY 243 AAGCGGCGACTGAGGCGCTGTGTCAGCGCATCAAGAACCCCGACGTGCGCGAGCTGCTG 302
DB 64 AAGCGGCGACTGAGGCGCTGTGTCAGCGCATCAAGAACCCCGACGTGCGCGAGCTGCTG 123
QY 303 ACCGAGATCTTCATGAAGACCCCGAGAGAGAGATTTCATGCAAGCGGTGCGGAGGTG 362
DB 124 ACCGAGATCTTCATGAAGACCCCGAGAGAGAGATTTCATGCAAGCGGTGCGGAGGTG 183
QY 363 GCCGCTCCCTGCAAGCGCGTGTTCAGAGAGCGCCCGAGAGTGTCCCATCTTCAAGCAG 422
DB 184 GCCGCTCCCTGCAAGCGCGTGTTCAGAGAGCGCCCGAGAGTGTCCCATCTTCAAGCAG 243
QY 423 ATCGTTAGCTGAGCGCGTGTATCACTTCCGCGTGTCTGTGCTGAGCAGCGCGGCAAC 482
DB 244 ATCGTTAGCTGAGCGCGTGTATCACTTCCGCGTGTCTGTGCTGAGCAGCGCGGCAAC 303
QY 483 CTGCAAGTCAACCGGCGCTTCCGCGTGTGAGTACTGTGCTGCGGCGCTTCAAGAGGC 542
DB 304 CTGCAAGTCAACCGGCGCTTCCGCGTGTGAGTACTGTGCTGCGGCGCTTCAAGAGGC 363
QY 543 GCGCTGCGCTTCAACCGCTCGTGAAGCTGTTCATCATGAAGTCTTGGCTTTGAGCAG 602
DB 364 GCGCTGCGCTTCAACCGCTCGTGAAGCTGTTCATCATGAAGTCTTGGCTTTGAGCAG 423

QY 603 ATCTTCAAGAACAGCTTACACACCTGCGCATAGGGCGGCGGCAAGGGCGCTCCGACTTC 662
DB 424 ATCTTCAAGAACAGCTTACACACCTGCGCATAGGGCGGCGGCAAGGGCGCTCCGACTTC 483
QY 663 GACCCCAAGGGCAAGAGGAGCGCGAGGTGATGCGCTTCTCCAGTCTCTTCAATGACCGAG 722
DB 484 GACCCCAAGGGCAAGAGGAGCGCGAGGTGATGCGCTTCTCCAGTCTCTTCAATGACCGAG 543
QY 723 CTGAGCGCCCATCATAGCTACGTGCAAGAGCGTCCCGCGGCGACATCGCGGTGCGCG 782
DB 544 CTGAGCGCCCATCATAGCTACGTGCAAGAGCGTCCCGCGGCGACATCGCGGTGCGCG 603
QY 783 CGCGAGATTGGCTACCTTTTCCGCGAGTACAGAGGCGATCAACCAAGACTAAGCGCGTG 842
DB 604 CGCGAGATTGGCTACCTTTTCCGCGAGTACAGAGGCGATCAACCAAGACTAAGCGCGTG 663
QY 843 CTGACCCCGAAGGGCCAGAGATATGCGCGCTCCGAGATCCGCCCGAGGCCACCGGCTAC 902
DB 664 CTGACCCCGAAGGGCCAGAGATATGCGCGCTCCGAGATCCGCCCGAGGCCACCGGCTAC 723
QY 903 GCGCGCTGTGCTTTTGTGAGAACGTGCTGAAGACAAAGGCGAGAGCTTCAAGGGCAAG 962
DB 724 GCGCGCTGTGCTTTTGTGAGAACGTGCTGAAGACAAAGGCGAGAGCTTCAAGGGCAAG 783
QY 963 CGCTGCTGTGTGTCTGCGCGCGGCGACAGTGGCCCAAGTACTGCGGAGCTGTCTGAG 1022
DB 784 CGCTGCTGTGTGTCTGCGCGCGGCGACAGTGGCCCAAGTACTGCGGAGCTGTCTGAG 843
QY 1023 AAGGGCGCATCGTGTGTGCTGCTGCTGCCATCCAGGGGCTACGTGTACAGCCCAAGCGC 1082
DB 844 AAGGGCGCATCGTGTGTGCTGCTGCTGCCATCCAGGGGCTACGTGTACAGCCCAAGCGC 903
QY 1083 TTCAAGCGCGAGCAGCTGTCAGAGCGGTGCAAGACATGAAGAAAGAACCAAGCGCCGC 1142
DB 904 TTCAAGCGCGAGCAGCTGTCAGAGCGGTGCAAGACATGAAGAAAGAACCAAGCGCCGC 963
QY 1143 ATCTCCAGATCAAGAGCGACACCGCGTGTATGTGGCGCACCGCGGACCTTTGGAG 1202
DB 964 ATCTCCAGATCAAGAGCGACACCGCGTGTATGTGGCGCACCGCGGACCTTTGGAG 1023
QY 1203 CTGAGTGGCGAGGTGAGCATGCGCTTCCCGCGGCGCACCCGAGAGAGATGATGAGCAG 1262
DB 1024 CTGAGTGGCGAGGTGAGCATGCGCTTCCCGCGGCGCACCCGAGAGAGATGATGAGCAG 1083
QY 1263 GACGCGGAGCTGTATCAAGCAGCGCTGCCAGTACGTGTGAGGGCGGCCAATGCGCC 1322
DB 1084 GACGCGGAGCTGTATCAAGCAGCGCTGCCAGTACGTGTGAGGGCGGCCAATGCGCC 1143
QY 1323 TTCAACCAAGAGGCGATTCACAGTACAAAGGCGCGCATCATCTACTGCGCGGCAAG 1382
DB 1144 TTCAACCAAGAGGCGATTCACAGTACAAAGGCGCGCATCATCTACTGCGCGGCAAG 1203
QY 1383 GCGGCGCAACCGCGCGCGGTGCGGTGAGCGGCGCTGAGAGTACCGCAACCGGATGAGC 1442
DB 1204 GCGGCGCAACCGCGCGCGGTGCGGTGAGCGGCGCTGAGAGTACCGCAACCGGATGAGC 1263
QY 1443 CTGAAGTGAAGTCCGCGAGAGGTTCGAGCAAGAGCTGAGCGCATCATGAAGACATCTAC 1502
DB 1264 CTGAAGTGAAGTCCGCGAGAGGTTCGAGCAAGAGCTGAGCGCATCATGAAGACATCTAC 1323
QY 1503 GACTCCGCGATGAGGCGGTTCGCGAGATACATATTTGACTGTGCGGCGCGCAATC 1562
DB 1324 GACTCCGCGATGAGGCGGTTCGCGAGATACATATTTGACTGTGCGGCGCGCAATC 1383
QY 1563 GCGGCGCTTCAACAGGAGGTGATGCGGTCAAGGCGCGGCGGTGTTAAGCTGCGCAG 1622
DB 1384 GCGGCGCTTCAACAGGAGGTGATGCGGTCAAGGCGCGGCGGTGTTAAGCTGCGCAG 1443
QY 1623 GCCCAAGCAGCGGCTCAACCGGCAATCCAC 1652
DB 1444 GCCCAAGCAGCGGCTCAACCGGCAATCCAC 1473

RESULT 14
US-08-828-451-25
Sequence 25, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanichik & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1431
US-08-828-451-25

Query Match 68.7%; Score 1470; DB 2; Length 1473;
Best Local Similarity 100.0%; Pred. No. 4,1e-289;
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 ATGACGCGCACACCGGCGGACTTCAACGCGCTGCGAGAGGCGGTGAAGCAGATGAGCCACC 242
DB 4 ATGACGCGCACACCGGCGGACTTCAACGCGCTGCGAGAGGCGGTGAAGCAGATGAGCCACC 63
QY 243 AAGGCGGCGACTGAGGCGCTGTGTGACGCGCATCAAGAAACCCCGAGTGGCGGAGCTGTG 302
DB 64 AAGGCGGCGACTGAGGCGCTGTGTGACGCGCATCAAGAAACCCCGAGTGGCGGAGCTGTG 123
QY 303 ACCGAGATCTTCATGAAGAACCCCGAGGAGGAGGTTTCATGCAAGGCGGTGGCGGAGGTG 362
DB 124 ACCGAGATCTTCATGAAGAACCCCGAGGAGGAGGTTTCATGCAAGGCGGTGGCGGAGGTG 183
QY 363 GCGGCTCTCTGCAAGCCGCTGTTGAGAGAGCCCGGAGTGTGCGCCATCTTCAAGCAG 422
DB 184 GCGGCTCTCTGCAAGCCGCTGTTGAGAGAGCCCGGAGTGTGCGCCATCTTCAAGCAG 243
QY 423 ATCTGTGAGCTGAGGCGGTGATCACTTCCGCGGTCTCTGCTGAGAGCAGCGCGCAAC 482
DB 244 ATCTGTGAGCTGAGGCGGTGATCACTTCCGCGGTCTCTGCTGAGAGCAGCGCGCAAC 303

QY 483 CTGCAAGTCAACCGGCGCTTCCGCGTGCAGTACTGTCGCCATCGGCCCTTCAAGGCG 542
DB 304 CTGCAAGTCAACCGGCGCTTCCGCGTGCAGTACTGTCGCCATCGGCCCTTCAAGGCG 363
QY 543 GCGCTGGCTTCAACCCCTTCCGTAACCTGTTCATCAATGAAGTTCTTCTTGTAGCAG 602
DB 364 GCGCTGGCTTCAACCCCTTCCGTAACCTGTTCATCAATGAAGTTCTTCTTGTAGCAG 423
QY 603 ATCTTCAAGAACGCTTCAACCCCTTCCGTAACCTGTTCATCAATGAAGTTCTTCTTGTAGCAG 662
DB 424 ATCTTCAAGAACGCTTCAACCCCTTCCGTAACCTGTTCATCAATGAAGTTCTTCTTGTAGCAG 483
QY 663 GACCCCAAGGCGCAAGAGCGAGCGAGGATCGCTTTCGCAAGTCTTCAATGACCGAG 722
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QY 843 CTGACCCCGAAGGCGCAGAGATGCGCGCTCCGAGATCCGCCCGAGGCGCAACCGGCTAC 902
DB 664 CTGACCCCGAAGGCGCAGAGATGCGCGCTCCGAGATCCGCCCGAGGCGCAACCGGCTAC 723
QY 903 GCGCGCTGCTGTTTGTGAGAACTGTCTGAGAGCAAGGCGCAAGGCTTCAAGGCGCAAG 962
DB 724 GCGCGCTGCTGTTTGTGAGAACTGTCTGAGAGCAAGGCGCAAGGCTTCAAGGCGCAAG 783
QY 963 CGCTGCTGTGTGTGCGCGCGCGCAAGTGTGCGCGCAAGTGTGCGCGCGCTGTGAG 1022
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DB 844 AAGGCGCGCATGCGTGTGCTGTGCGCTGTGCGCTGTGCGCGCGCATGCGTGTGAG 903
QY 1083 TTCAAGGCGGAGCAGCTGAGGCGGTGCGAGAGATGAAGAAAGAAACAAGCGCGCG 1142
DB 904 TTCAAGGCGGAGCAGCTGAGGCGGTGCGAGAGATGAAGAAAGAAACAAGCGCGCG 963
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RESULT 15

US-09-252-991A-4131/c
; Sequence 4131, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4131
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4131

Query March 27.7%; Score 592.2; DB 4; Length 1497;

Best Local Similarity 68.1%; Pred. No. 6.1e-111; Mismatches 889; Conservative 0; Indels 18; Gaps 4;

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Job time : 388 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2005, 19:09:08 ; Search time 1204 Seconds
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Title: US-10-627-886-1

Perfect score: 2140

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Scoring table: IDENTITY NUC

Gap: 10.0 , Gapext 1.0

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

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Listing first 45 summaries

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Published Applications NA:*

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- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2140	100.0	2140	9	US-10-627-886-1
3	2137	99.9	2137	9	US-09-070-844-18
4	2137	99.9	2137	19	US-10-627-886-18
5	2046	95.6	2099	9	US-09-070-844-3
6	2046	95.6	2099	19	US-10-627-886-3
7	2043	95.5	2096	9	US-09-070-844-19

8	2043	95.5	2096	19	US-10-627-886-19	Sequence 19, Appl
9	1969	92.0	1969	9	US-09-070-844-7	Sequence 7, Appl
10	1969	92.0	1969	9	US-10-627-886-7	Sequence 23, Appl
11	1501.4	70.2	1506	9	US-09-070-844-23	Sequence 23, Appl
12	1501.4	70.2	1506	19	US-10-627-886-23	Sequence 23, Appl
13	1470	68.7	1473	9	US-09-070-844-25	Sequence 25, Appl
14	1470	68.7	1473	19	US-10-627-886-25	Sequence 25, Appl
15	590.8	27.6	1338	17	US-10-282-122A-30503	Sequence 30503, A
16	572.4	26.7	2256646	19	US-10-470-565-1	Sequence 1, Appl
17	529.2	24.7	1392	17	US-10-282-122A-15094	Sequence 15094, A
18	526.2	24.6	1347	17	US-10-282-122A-31354	Sequence 31354, A
19	508.2	23.7	1275	17	US-10-369-493-24304	Sequence 24304, A
20	500.4	23.4	1314	17	US-10-369-493-34308	Sequence 34308, A
21	499.8	23.4	1335	17	US-10-369-493-37634	Sequence 37634, A
22	488.6	22.8	1332	17	US-10-282-122A-28945	Sequence 28945, A
23	472.6	22.1	1335	17	US-10-282-122A-151	Sequence 151, App
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25	460.8	21.5	1344	17	US-10-369-493-31902	Sequence 31902, A
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32	415.8	19.4	1344	17	US-10-282-122A-39409	Sequence 39409, A
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41	341	15.9	12666	8	US-08-961-527-137	Sequence 137, App
42	341	15.9	12666	17	US-10-158-844-137	Sequence 137, App
43	340.4	15.9	2162598	21	US-10-472-928-49579	Sequence 49579, A
44	338.2	15.8	1341	17	US-10-369-493-44956	Sequence 44956, A
45	337.4	15.8	1344	17	US-10-282-122A-42104	Sequence 42104, A

ALIGNMENTS

RESULT 1
US-09-070-844-1
Sequence 1, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/070, 844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1610
US-09-070-844-1

Query Match 100.0%; Score 2140; DB 9; Length 2140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2041 AGTGTGCGTGCCTTGCCTCGCGCTGCCCGGAGTGGATCTGTGACCTGAGAGGCTTGT 2100
2041 AGTGTGCGTGCCTTGCCTCGCGCTGCCCGGAGTGGATCTGTGACCTGAGAGGCTTGT 2100
2101 GTAAACACGACGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2140
2101 GTAAACACGACGAGCTCAAAAAAAAAAAAAAAAAAAAAA 2140
RESULT 2
US-10-627-886-1
Sequence 1, Application US/10627886
Publication No. US20040126710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1610

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Query Match	100.0%;	Score 2140;	DB 19;	Length 2140;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2140;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	CTCCCTTCCTGCTGCGCCCTCTCTCCGTCGCCGCAATGACAGACCGCCCTGTGCGCCAAAGCTTA	60		
DB 1	CTCCCTTCCTGCTGCGCCCTCTCTCTCCGTCGCCGCAATGACAGACCGCCCTGTGCGCCAAAGCTTA	60		
QY 61	TCGTGACGCGCCCGCCTGTGAGCGGCAAGCGCCGCGCTCTCTGCGCGCTGTGCGCGCTGAGG	120		
DB 61	TCGTGACGCGCCCGCCTGTGAGCGGCAAGCGCCGCGCTCTCTGCGCGCTGTGCGCGCTGAGG	120		
QY 121	TCGCGCTCCGCGCAAGCGCGATGTCCGCGCCAAAGCGCGTCTGCGCTTGAAGAGCAGATCTTCG	180		
DB 121	TCGCGCTCCGCGCAAGCGCGATGTCCGCGCCAAAGCGCGTCTGCGCTTGAAGAGCAGATCTTCG	180		
QY 181	CGATGAGAGCCCAACACCGGCGCATTTCAACGCGCGCTGCAAGAGGCGGTGAAGCATGTGCCA	240		
DB 181	CGATGAGAGCCCAACACCGGCGCATTTCAACGCGCGCTGCAAGAGGCGGTGAAGCATGTGCCA	240		
QY 241	CCAAGGCGGGGCACTGAAGGCGCTGTGAGACGGGCATCAAGAAACCGGACGCTGCGCAGCTGC	300		
DB 241	CCAAGGCGGGGCACTGAAGGCGCTGTGAGACGGGCATCAAGAAACCGGACGCTGCGCAGCTGC	300		
QY 301	TGACCGAGATCTTCATGAAGGACCCCGGACGACGAGATTTCATGACGCGGTGCGCGAGG	360		
DB 301	TGACCGAGATCTTCATGAAGGACCCCGGACGACGAGATTTCATGACGCGGTGCGCGAGG	360		
QY 361	TGCGCGTCTCCCTGACGCGCGGTGTTGAGAAAGCGCCCGAGCTGCTGCCATCTTCAAGC	420		
DB 361	TGCGCGTCTCCCTGACGCGCGGTGTTGAGAAAGCGCCCGAGCTGCTGCCATCTTCAAGC	420		
QY 421	AGATCGTTGAGCCCTGAACCGGTGATTCACCTTCGCGGTCTCTGCGTGAAGACCGCGGCA	480		
DB 421	AGATCGTTGAGCCCTGAACCGGTGATTCACCTTCGCGGTCTCTGCGTGAAGACCGCGGCA	480		
QY 481	ACCTGACAGATCAACCGGCGCTTCGCGGTGACGATCTGTCCGCGCATCGGCCCTTCAAGG	540		
DB 481	ACCTGACAGATCAACCGGCGCTTCGCGGTGACGATCTGTCCGCGCATCGGCCCTTCAAGG	540		
QY 541	GCGGCGTGCCTTCACCCCTCGGTGAACCTGTGCATCATGAAGTCTCTTGCTTTGAGC	600		
DB 541	GCGGCGTGCCTTCACCCCTCGGTGAACCTGTGCATCATGAAGTCTCTTGCTTTGAGC	600		
QY 601	AGATCTTCAAGAACGCTTGACCAACCTTGCCCATGAGGCGGCGGCAAGGCGCGCTCCGACT	660		
DB 601	AGATCTTCAAGAACGCTTGACCAACCTTGCCCATGAGGCGGCGGCAAGGCGCGCTCCGACT	660		
QY 661	TCGACCCCAAGGGCAAGAGGAGCGCGGAGGTGATGCGCTTCTGCAAGTCTTCAATGACG	720		
DB 661	TCGACCCCAAGGGCAAGAGGAGCGCGGAGGTGATGCGCTTCTGCAAGTCTTCAATGACG	720		
QY 721	AGCTGACAGCGCATCATGACTGTGAGGACGTCGCCGCGCGAGCATCGGCTGTGAGCG	780		
DB 721	AGCTGACAGCGCATCATGACTGTGAGGACGTCGCCGCGCGAGCATCGGCTGTGAGCG	780		
QY 781	CGGCGAGATTGAGCTATCTTTTCGCGCAATCAAGGCGCATCAACCAAGACTCAACCGGCG	840		
DB 781	CGGCGAGATTGAGCTATCTTTTCGCGCAATCAAGGCGCATCAACCAAGACTCAACCGGCG	840		
QY 841	TGCTGACCCCGGCAAGGCGCAAGAGATGCGCGCTCCGAGATCCGCGCCGAGGCGCACCGGCT	900		
DB 841	TGCTGACCCCGGCAAGGCGCAAGAGATGCGCGCTCCGAGATCCGCGCCGAGGCGCACCGGCT	900		
QY 901	ACGCGCGCGTGTCTTTGTGAGAGACGTGTGAAAGCAAGGCGGAGAGCTTCAAGGCGCA	960		
DB 901	ACGCGCGCGTGTCTTTGTGAGAGACGTGTGAAAGCAAGGCGGAGAGCTTCAAGGCGCA	960		
QY 961	AGCGCTGCTGTGTGTGTGCGCGCGGCAACGTGACCAATGACTGTGCGGAGCTGTGCTGG	1020		
DB 961	AGCGCTGCTGTGTGTGTGCGCGCGGCAACGTGACCAATGACTGTGCGGAGCTGTGCTGG	1020		

Db 241 AGGGGGGAGCTGAGGGCCCTGGTGCAACGGGCTTAAGAACCCCGAAGCTGGCCGAGCTGCTGA 300
Qy 304 CCGAGATTTTCAATGAAGAACCCCGAGAGCAAGAGATTCAATGAGGCGGTGGCCGAGGTGG 363
Db 301 CCGAGATTTTCAATGAAGAACCCCGAGAGCAAGAGATTCAATGAGGCGGTGGCCGAGGTGG 360
Qy 364 CCGTCTCCCTGAGCCCGTGTTCGAGAACCCCGAGAGCTGCTGGCCATTTTCAAGAGCA 423
Db 361 CCGTCTCCCTGAGCCCGTGTTCGAGAACCCCGAGAGCTGCTGGCCATTTTCAAGAGCA 420
Qy 424 TCGTTGAGCCTGAGCGCTGATCACTTCGCGGTTCCTGGCTGAGACAGCCGGCAACC 483
Db 421 TCGTTGAGCCTGAGCGCTGATCACTTCGCGGTTCCTGGCTGAGACAGCCGGCAACC 480
Qy 484 TGCAGTCAACCGCGGCTTCCGCGTGCAAGTACTGTCGCCATTCGCGCCCTTAACAAGGCG 543
Db 481 TGCAGTCAACCGCGGCTTCCGCGTGCAAGTACTGTCGCCATTCGCGCCCTTAACAAGGCG 540
Qy 544 GCGTGGCGTTCAACCCCTCCGAGAACCTGTCATCATAGTTCCTTTCCTTTGAGCAGA 603
Db 541 GCGTGGCGTTCAACCCCTCCGAGAACCTGTCATCATAGTTCCTTTCCTTTGAGCAGA 600
Qy 604 TCTTCAAGAGAGCTGACCAACCTGCGCATGAGCGGCGCAAGGCGGCTCCGACTTCG 663
Db 601 TCTTCAAGAGAGCTGACCAACCTGCGCATGAGCGGCGCAAGGCGGCTCCGACTTCG 660
Qy 664 ACCCAAGGAGGAGAGGAGCGAGAGTGAATGCGCTTTCGCAAGTCTTCAATGACAGAGC 723
Db 661 ACCCAAGGAGGAGAGGAGCGAGAGTGAATGCGCTTTCGCAAGTCTTCAATGACAGAGC 720
Qy 724 TGCAGCGGCAATCAAGTACGTGCAAGAGAGTCCCGCGGCGCAATCGGCGGTGGCGGC 783
Db 721 TGCAGCGGCAATCAAGTACGTGCAAGAGAGTCCCGCGGCGCAATCGGCGGTGGCGGC 780
Qy 784 GCGAGATTGGCTACCTTTTCGAGCAGTACAGCGCATCAACCAAGACTCAACCGGCGTGC 843
Db 781 GCGAGATTGGCTACCTTTTCGAGCAGTACAGCGCATCAACCAAGACTCAACCGGCGTGC 840
Qy 844 TGACCCCGAGAGGAGGAGAGTATGGCGGCTCCGAGATCCGCCCGAGGCAACCGGCTACG 903
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Qy 904 GCGCGGTCTGTTTGTGAGAACTGCTGAGAGAGCAAGGCGAGAGCTCAAGGCGCAAGC 963
Db 901 GCGCGGTCTGTTTGTGAGAACTGCTGAGAGAGCAAGGCGAGAGCTCAAGGCGCAAGC 960
Qy 964 GCTGCTGTGTGCTGAGCGGAGCAAGTGGCCAGTACTGCGCGGAGGCTGCTGAGAGA 1023
Db 961 GCTGCTGTGTGCTGAGCGGAGCAAGTGGCCAGTACTGCGCGGAGGCTGCTGAGAGA 1020
Qy 1024 AGGGGCGCATGCTGTGCTGCTGCTGCACTCCAGAGGCTACGTGTACAGGCGCAACGCT 1083
Db 1021 AGGGGCGCATGCTGTGCTGCTGCTGCACTCCAGAGGCTACGTGTACAGGCGCAACGCT 1080
Qy 1084 TCAGCGCGGAGAGCTGAGAGCGGTGAGAGACATGAAGAAAGAAACAACGCGCGCCA 1143
Db 1081 TCAGCGCGGAGAGCTGAGAGCGGTGAGAGACATGAAGAAAGAAACAACGCGCGCCA 1140
Qy 1144 TCTCCAGATACAAAGAGAGCAACCGCGGTATGTTGGGAGACCGCGCAAGGCTTTGGAGC 1203
Db 1141 TCTCCAGATACAAAGAGAGCAACCGCGGTATGTTGGGAGACCGCGCAAGGCTTTGGAGC 1200
Qy 1204 TGAAGTGCAGGTGAGACATCGCTTCCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1263
Db 1201 TGAAGTGCAGGTGAGACATCGCTTCCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Qy 1264 AGCGGAGCTGTGATCAAGAGCGGCTGCGAGTACGTGTGAGAGGCGGCAACATGCTCT 1323
Db 1261 AGCGGAGCTGTGATCAAGAGCGGCTGCGAGTACGTGTGAGAGGCGGCAACATGCTCT 1320
Qy 1324 CCACCAAGAGGAGGAGTCAAGAGTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1383

Db 1321 CCACCAAGAGGAGGAGTCAAGAGTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
Qy 1384 CCGCCAAAGCGCGGCGGTGGCTGAGCGGCTGAGAGATGAACCAAGAACCGCATGAGCC 1443
Db 1381 CCGCCAAAGCGCGGCGGTGGCTGAGCGGCTGAGAGATGAACCAAGAACCGCATGAGCC 1440
Qy 1444 TGAAGTGCAGGTGAGAGGAGTGGAGCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1503
Db 1441 TGAAGTGCAGGTGAGAGGAGTGGAGCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1500
Qy 1504 ACTCGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1563
Db 1501 ACTCGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Qy 1564 CCGGCTTCAACCAAGTGTGATGCTGCAAGGCGGAGGCGGCTGTTTAACTGAGCTCCAGG 1623
Db 1561 CCGGCTTCAACCAAGTGTGATGCTGCAAGGCGGAGGCGGAGGCGGCTGTTTAACTGAGCTCCAGG 1620
Qy 1624 CCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1683
Db 1621 CCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
Qy 1684 AAGCGGCGCTTTTTCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1743
Db 1681 AAGCGGCGCTTTTTCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
Qy 1744 GCGGTGCGCTGCAATTCACCCCAAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1803
Db 1741 GCGGTGCGCTGCAATTCACCCCAAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
Qy 1804 CTATTTTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1863
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Qy 1864 GAGCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1923
Db 1861 GAGCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
Qy 1924 CTTGTTGAGAGGCTTACAGGCTCAATTCCTTTTATGATGAGGAGGAGGAGGAGGAGGAGG 1983
Db 1921 CTTGTTGAGAGGCTTACAGGCTCAATTCCTTTTATGATGAGGAGGAGGAGGAGGAGGAGG 1980
Qy 1984 CGAATTTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2043
Db 1981 CGAATTTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
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Db 2041 GTGCGTGCCTTGCCTGCGCTGCGCGGAGTGCATCTGTGAGAGTGTGTGTA 2100
Qy 2104 AACACGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2140
Db 2101 AACACGAGAGTCAAAAAAAAAAAAAAAAAAAAAA 2137

RESULT 4
US-10-627-886-18
; Sequence 18, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanichik & Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-627-886-18

Query Match 99.9%; Score 2137; DB 19; Length 2137;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CTTTCTGTCGACCTCTCTCCGTCGCCCATGACAGCCGCTCTGTCGCAAGCTTATCG 63
1 CTTTCTGTCGACCTCTCTCCGTCGCCCATGACAGCCGCTCTGTCGCAAGCTTATCG 60
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61 TGGCCGCGCGCTGAGCGGACGCGCGCTGCTCGCGCGCTGCGCGCTGCGCTGCGTCC 120
124 GCTCCGCGCAAGCGGATGTCGCGCGCAAGCGCGCTGCTGCGCGCGCTGCGCGCGTCC 183
121 GCTCCGCGCAAGCGGATGTCGCGCGCAAGCGCGCTGCTGCGCGCGCTGCGCGCGTCC 180
184 TGAACGCCACCAACCGGCGATTCACAGCGCTGACAGAAAGCGGTGAAGAGATGCGACA 243
181 TGAACGCCACCAACCGGCGATTCACAGCGCTGACAGAAAGCGGTGAAGAGATGCGACA 240
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241 AGCGCGGCGATGAGGCGCTGCTGCAAGCGCATCAAGAACCCGACGTCGCGCATGCTGA 300
304 CCGAGATCTTCATGAGGACCCGAGGACGAGAGATTCATGACGCGGTGCGAGGTCG 363
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364 CCGCTCTCCCTGACAGCCGCTGTTGCAAGAGCGCCCGAGCTGCTCCCATCTTCAAGCGA 423
361 CCGCTCTCCCTGACAGCCGCTGTTGCAAGAGCGCCCGAGCTGCTCCCATCTTCAAGCGA 420
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484 TGCAGGTCAACCGGCGCTTCCGCGTGAAGTACTGTCGCGCATGCGGCCCTTAAGAGGCG 543
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661 ACCCCAGGCGCAAGAGCGCGGAGGTGATGCGCTTCTGCAATCCTTCATGACCGAGC 720
724 TGCAGCGCACATCAAGTACGTCAGGACGTCGCCCGCGCGCATGCGCGCGCGCGC 783
721 TGCAGCGCACATCAAGTACGTCAGGACGTCGCCCGCGCGCATGCGCGCGCGCGC 780
784 GCGAGATTGGCTACCTTTTGGCCAGTACAGGCGCATCAACCAAGAACTAACCGGCGTCG 843
781 GCGAGATTGGCTACCTTTTGGCCAGTACAGGCGCATCAACCAAGAACTAACCGGCGTCG 840
844 TGACCCCGAAGGCGCAGAGTATGCGCGCTCCGAGATCCGCGCGCGAGCGCACCGGCTACG 903
841 TGACCCCGAAGGCGCAGAGTATGCGCGCTCCGAGATCCGCGCGCGAGCGCACCGGCTACG 900
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901 GCGCGGTGCTGTTTGTGAGAACGTCGTGAAGAACAGGCGAGCTTCAAGGCGCAAGC 960
964 GCTGCTGTGTCTGTGCGCGCGCGCAAGTGGCCCAAGTCTGCGCGGAGCTCTGTGAGA 1023
961 GCTGCTGTGTCTGTGCGCGCGCGCAAGTGGCCCAAGTCTGCGCGGAGCTCTGTGAGA 1020
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1021 AGGCGGCATCGTGTGCTGCTGCTGCGCACTCCAGAGGCTACGTACGAGCCCAACG 1080
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1081 TCAAGCGCGAGCAGCTGACAGCGGTCGAGGACATGAAGAAAGAACCAACAGCGCCGCA 1140
1144 TCTCCGAGTCAAGAGCGACACCGCGGTATGTGGCGCACCGCGCAACCTTTGGAGC 1203
1141 TCTCCGAGTCAAGAGCGACACCGCGGTATGTGGCGCACCGCGCAACCTTTGGAGC 1200
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1201 TGAAGTGCAGGTGAGCATGCGCTTCCCTGCGCACCCAGAAAGAGATGATGAGCAGC 1260
1264 AGCGCGAGCTGTGATCAAGCAGCGCTGCGAGTACGTGTGAGAGGCGCAACATGCTCT 1323
1261 AGCGCGAGCTGTGATCAAGCAGCGCTGCGAGTACGTGTGAGAGGCGCAACATGCTCT 1320
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1321 CCAACCAAGAGCGCATCAAGTCAACAAAGCGCGCGCATCTATGCGCGCGCAAG 1380
1384 CCGGCAACGCGCGCGCGCTGAGCGCTGAGAGTGAACCCAGAACCGAGTGAAGC 1443
1381 CCGGCAACGCGCGCGCGCTGAGCGCTGAGAGTGAACCCAGAACCGAGTGAAGC 1440
1444 TGAATTGAGTTCGAGAGAGTTCGCGAACAGCTGAGCGCATCATGAAGACATCTTACG 1503
1441 TGAATTGAGTTCGAGAGAGTTCGCGAACAGCTGAGCGCATCATGAAGACATCTTACG 1500
1504 ACTTCGCGCATGAGGCGCTCCCGAGATCAATGTTGACTGTGCGCGCGCGCAACATCG 1563
1501 ACTTCGCGCATGAGGCGCTCCCGAGATCAATGTTGACTGTGCGCGCGCGCAACATCG 1560
1564 CCGGCTTCAACCAAGGTGATGCGCTCAAGGCGCGCGCGCTTTTAAGTGTCCAGG 1623
1561 CCGGCTTCAACCAAGGTGATGCGCTCAAGGCGCGCGCGCTTTTAAGTGTCCAGG 1620
1624 CCAAGCGCAGGCTACCGGCAATCCAAACCAACCTCAAGCGCGCAAGCCTTTTCGG 1683

1621 CCCAAGCCACGGCTACCGGCAATCAACCACTCAACGCGGCAAGCTTTGG 1680
1684 AAGGGGCGCTTTTCCAGCCAGGCGCTCACTGCGCTTCAATACCTGCTAATGCC 1743
1681 AAGGGGCGCTTTTCCAGCCAGGCGCTCACTGCGCTTCAATACCTGCTAATGCC 1740
1744 GCGGCGCGCTTCAATTCACCCCAAGAAAGAACTAGCGGCACTGATGATCAAGGACG 1803
1741 GCGGCGCGCTTCAATTCACCCCAAGAAAGAACTAGCGGCACTGATGATCAAGGACG 1800
1804 CTATTTTTCGCGACGCGGCGCTCAACCCGAGGCTTCTCCCGAGCCCTAAGCGCT 1863
1801 CTATTTTTCGCGACGCGGCGCTCAACCCGAGGCTTCTCCCGAGCCCTAAGCGCT 1860
1864 GACGTCGCGCGGCTTCTGCGATGCGCTCGGTTTGAACCCCTCACTGATCAACGAC 1923
1861 GACGTCGCGCGGCTTCTGCGATGCGCTCGGTTTGAACCCCTCACTGATCAACGAC 1920
1924 CCGTGTGAAGCGCTACAGGCTCAATGCGCTTATAGTGTAGCGCGCGCGCGCGCG 1983
1921 CCGTGTGAAGCGCTACAGGCTCAATGCGCTTATAGTGTAGTGTAGCGCGCGCGCG 1980
1984 GGAATTTTCCTGCGATGAGAGCGTGGGTTCTTACGCTGCTGACCCCAAGTAGAGTAGT 2043
1981 GGAATTTTCCTGCGATGAGAGCGTGGGTTCTTACGCTGCTGACCCCAAGTAGAGTAGT 2040
2044 GTGCGTGTGCTGCGCTGCGCTGCGCGGATGCGATGCTGATGCTGAGAGTGTGTGTA 2103
2041 GTGCGTGTGCTGCGCTGCGCTGCGCGGATGCGATGCTGATGCTGAGAGTGTGTGTA 2100
2104 AACGACGAGTCAAAAAA 2140
2101 AACGACGAGTCAAAAAA 2137

RESULT 5
US-09-070-844-3
Sequence 3, Application US/09070844
Patent No. US2002062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanhik & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070, 844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2099 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 33..1568
US-09-070-844-3
Query Match 95.6%; Score 2046; DB 9; Length 2099;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
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1 CTCCTTTCTGCTGCGCTCTCTGCGCGGCAATGACAGCGGCTGCGGCAAGCTTA 60
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79 TCGGCTGCGGCAAGCGGCGGATGCGGCGGCAAGCGGCGGCTGCGGCGGCGGCGG 138
181 CGATGACGCGCACACCGCGGAGCTTCAAGCGGCTGCGGCAAGCGGCGGCGGCGG 240
139 CGATGACGCGCACACCGCGGAGCTTCAAGCGGCTGCGGCAAGCGGCGGCGGCGG 198
241 CCAAGCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
199 CCAAGCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258
301 TGAACGAGATCTTCATGAGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
259 TGAACGAGATCTTCATGAGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 318
361 TGGCGGCTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
319 TGGCGGCTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 378
421 AGATCTTGAAGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
379 AGATCTTGAAGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 438
481 ACCGCGAGTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
439 ACCGCGAGTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 498
541 GCGGCGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
499 GCGGCGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 558
601 AGATCTTGAAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
559 AGATCTTGAAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 618
661 TCGAACCAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
619 TCGAACCAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678
721 AGCTGACGCGCACATCACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 780
679 AGCTGACGCGCACATCACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 738
781 CGGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
739 CGGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798
841 TGCAGACCCGGAAGGCGGCGGAGATGAGCGGCTGCGAGATCGGCGCGGCGGCGG 900

US-09-070-844-19
; Sequence 19, Application US/09070844
; Patent No. US2002062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
; TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,844
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WhiteLock, Ted W.
; REGISTRATION NUMBER: 36,965
; REFERENCE/DOCKET NUMBER: UF155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-09-070-844-19

Query Match 95.5%; Score 2043; DB 9; Length 2096;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 4 CTTTCTGCTCGCCCTCTCTCCGTCGCCATGACAGACCGCCCTGCTGCGCCAAAGCTTATCG 63
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DB 61 TGGCC-----TGCCCGTGGGTCC 78
QY 124 GCTCGCGCAAGCGGATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGATCTCCGCGA 183
DB 79 GCTCGCGCAAGCGGATGTCGCGCGCAAGCGCGTCTGCTGAGAGAGATCTCCGCGA 138
QY 184 TGGACGCCACCGCGGCACTTCAACGCGCTGACAGAAAGCGGTGAAGAGATGACCA 243
DB 139 TGGACGCCACCGCGGCACTTCAACGCGCTGACAGAAAGCGGTGAAGAGATGACCA 198
QY 244 AGCGCGGCACTGAGGCGCTGTGTGCAACGCGCATCAAGAACCCGACGTCGCCAGCTGTGA 303
DB 199 AGCGCGGCACTGAGGCGCTGTGTGCAACGCGCATCAAGAACCCGACGTCGCCAGCTGTGA 258
QY 304 CCGAGATCTTATGAAGACCCGAGACGACGAGATTCATGACGCGGTGCGGAGGTGG 363
DB 259 CCGAGATCTTATGAAGACCCGAGACGACGAGATTCATGACGCGGTGCGGAGGTGG 318

QY 364 CCGTCTCTCGACGCCGCTTTCAGAGAGCGCCCGAGCTGTCGCCATCTTCAAGCAGA 423
DB 319 CCGTCTCTCGACGCCGCTTTCAGAGAGCGCCCGAGCTGTCGCCATCTTCAAGCAGA 378
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DB 379 TCGTTAGCCTGAGCGGTATACCTTCCGCGTGTCTGCTGGAGACGCGCGCAACC 438
QY 484 TGCAGGTCAACCGCGGCTTCGCGGTGACGACTGCTCCGCGCATCGGCGCTTCAAGGCG 543
DB 439 TGCAGGTCAACCGCGGCTTCGCGGTGACGACTGCTCCGCGCATCGGCGCTTCAAGGCG 498
QY 544 GCTCGCGCTTCAACCCCTCCGTGAACTGTCATCATGAAGTTCTTTCCTTTAGCAGA 603
DB 499 GCTCGCGCTTCAACCCCTCCGTGAACTGTCATCATGAAGTTCTTTCCTTTAGCAGA 558
QY 604 TCTTCAAGAACAGCTTGAACCACTTGGCCATGGGCGCGGCAAGGCGGCTCCGACTTCG 663
DB 559 TCTTCAAGAACAGCTTGAACCACTTGGCCATGGGCGCGGCAAGGCGGCTCCGACTTCG 618
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QY 724 TGCAGCGCAATCAGCTTACGTGACAGAGCGTGCCTCCGCGCGCAATCGGCGTGGCGCG 783
DB 679 TGCAGCGCAATCAGCTTACGTGACAGAGCGTGCCTCCGCGCGCAATCGGCGTGGCGCG 738
QY 784 GCGAGATTGGCTACCTTTTGGCCAGTACAAAGGCGATCAACAAAGTTACACCGCGCTGC 843
DB 739 GCGAGATTGGCTACCTTTTGGCCAGTACAAAGGCGATCAACAAAGTTACACCGCGCTGC 798
QY 844 TGAACCCGGAAGGCGCAGAGATATGCGCGCTCCGAGATCCGCGCGGAGGCGACCGCTACG 903
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QY 1204 TGGACTGCAAGTGAATCATGCGCTTCCCTGCGCCACCCAGAAAGAGATGATGAGCAGC 1263
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DB 1279 CCACCAACGAGGCGCATCAACAGTACAAAGGCGCGCATCATCTACTGCGCGGCAAGG 1338
QY 1384 CCGGCAACGCGCGGCGGTGCGCGGTCAAGCGGCTGAGATGACCCAGAAACCGCATGAGCC 1443
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QY 844 TGACCGCGAAGGCGCAGAGATATGCGGCTCCGAGATCCGCCCGAGGCGCACCGGCTACG 903
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QY 964 GCTGCTGCTGCTGCTGCGGCGGCGCAACGTCGCTGCTGCGGAGGCTGCTGCTGAGAGA 1023
Db 919 GCTGCTGCTGCTGCTGCGGCGGCGCAACGTCGCTGCTGCGGAGGCTGCTGCTGAGAGA 978
QY 1024 AGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
Db 979 AGGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
QY 1084 TCACGCGCGAGACGCTGACGCGCGTGCAGAGACATGAGAGAGAGAGAGAGAGAGAGAGAG 1143
Db 1039 TCACGCGCGAGACGCTGACGCGCGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
QY 1144 TCTCCGAGTACAG 1203
Db 1099 TCTCCGAGTACAG 1158
QY 1204 TGACGCTGCGAGTGAACATGCGCTTCCCTGCGGCGCACCGAGAGAGAGAGAGAGAGAG 1263
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QY 1264 AGCGCGAGCTCTGATCAAG 1323
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QY 1324 CCACCAACGAGGCGCATCCAGAGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
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QY 1384 CGGCGCAACGCGCGCGCTGCGGCTGACGCGGCTGAGAGATGACCCAGAGAGAGAGAGAG 1443
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Db 1399 TGAAGTGAATCTGCGGAG 1458
QY 1504 ACTCGCGCATGAGGCGCGCTGCGGAGTACAAAGTGTGACTGCGCGGCGGCGCAACATCG 1563
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QY 1564 CGGCGCTTCAACCAAGGCTGATGCGGCTGCAAGGCGCGAGAGAGAGAGAGAGAGAGAGAG 1623
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QY 1624 CCAGAGCAACGCTGACCGGCAATTCACCAACCAACTCAAGCGGCGAGAGAGAGAGAGAG 1683
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QY 1684 AAGGCGGCGCTTTTCCAGCGAGGCGCTGACCGGCGCTTCAATACCGGCTGATGCGC 1743
Db 1639 AAGGCGGCGCTTTTCCAGCGAGGCGCTGACCGGCGCTTCAATACCGGCTGATGCGC 1698

QY 1744 GCGGTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCGACTGATCAGACGCG 1803
Db 1699 GCGGTGCGCTGCAATTCACCCCAAGAGAACTAGCGGCGACTGATCAGACGCG 1758
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QY 1864 GAGTCCGCGCGACTTTCGCTGCGACATCGCTGCTGTTTGAACCCCTCCAGTACCCAC 1923
Db 1819 GAGTCCGCGCGACTTTCGCTGCGACATCGCTGCTGTTTGAACCCCTCCAGTACCCAC 1878
QY 1924 CTTGTTGAGACCTACACCTCAATTCCTTTTATGATGTCGCGCCCTCTGCGCCC 1983
Db 1879 CTTGTTGAGACCTACACCTCAATTCCTTTTATGATGTCGCGCCCTCTGCGCCC 1938
QY 1984 CGAATTTTCTGCGACATGAGAGCGGCTTCTGAGCTTGTGAGACCCCAAGAGAGAGTACT 2043
Db 1939 CGAATTTTCTGCGACATGAGAGCGGCTTCTGAGCTTGTGAGACCCCAAGAGAGAGTACT 1998
QY 2044 GTGCGTCTTTCGCTGCGCTGCGCGGAGATGAGATCTGAGACTGAGAGTCTTGCTA 2103
Db 1999 GTGCGTCTTTCGCTGCGCTGCGCGGAGATGAGATCTGAGACTGAGAGTCTTGCTA 2058
QY 2104 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
Db 2059 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2095

RESULT 9
US-09-070-844-7
Sequence 7, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanichik & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070, 844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-09-070-844-7

Query Match 92.0%; Score 1969; DB 9; Length 1969;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 291 GCGCAGCTGTGACCGGAGATCTTATGAAAGACCCGAGACGACAGAGATTCTACGAGCG 350
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Qy 351 GTGCGGAGGTGCGCGTCTCCCTGCGCGCGGTGTGAGAAAGCGCGCGAGCTGCTGCGC 410
Db 181 GTGCGGAGGTGCGCGTCTCCCTGCGCGCGGTGTGAGAAAGCGCGCGAGCTGCTGCGC 240
Qy 411 ATCTTCAAGCAGATGTTGAGCGCTGAGCGCGGTGATCACTTCCGCGTCTGTGCTGAGC 470
Db 241 ATCTTCAAGCAGATGTTGAGCGCTGAGCGCGGTGATCACTTCCGCGTCTGTGCTGAGC 300
Qy 471 GAGCGCGGCAACCTGAGAGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCGCATCGGC 530
Db 301 GAGCGCGGCAACCTGAGAGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCGCATCGGC 360
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Qy 891 GCGACCGGCTTACGGGCGCGTGTGTTTGTGAGAAACGTGCTGAAGAAAGGCGAGAC 950
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Qy 951 CTCAAGGCGCAAGCGCTGTGTGTCTGCGCGCGCAAGTGCCTCACTATCTGCGGAG 1010
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Qy 1011 CTGCTGTGAGAAAGGCGCATGTGTGTGTGCTGTCTGCACTCCAGGCGCTACGTGTAC 1070
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Db 1381 GCGCGCAACATCGCGGCTTACCAAGAGTGTGATGCGCTGCAAGGCGCGAGGCGCTGTT 1440
Qy 1611 TAAAGTGGCGGAGCGCAAGCGGCTCACCGGCAATCCAAACCAACATCAAGCGGC 1670
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Qy 1671 AAGACCTTTTGGAAAGGCGCGCTTTTCCAGCGAGGCGCTGACCTGCGCTTTCATTA 1730
Db 1501 AAGACCTTTTGGAAAGGCGCGCTTTTCCAGCGAGGCGCTGACCTGCGCTTTCATTA 1560
Qy 1731 CCTGTCTATTGCGCGCGTTCCTGTCGAATTCACCCCAAGAAAGTATGCGGCACTTGAC 1790
Db 1561 CCTGTCTATTGCGCGCGTTCCTGTCGAATTCACCCCAAGAAAGTATGCGGCACTTGAC 1620
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Db 1621 TGCAATGAGAGGCTATTTTGTGCGAGCGGCGCTCACCGCGAGGCTCTCTCCCGG 1680
Qy 1851 AGCCCTAAGCGCTGACGTCCGCCCGACTTGTGCTGCAATCGCTCGGTTTGAACCCCT 1910
Db 1681 AGCCCTAAGCGCTGACGTCCGCCCGACTTGTGCTGCAATCGCTCGGTTTGAACCCCT 1740
Qy 1911 CCACTTACCAACCTGTGTGAAAGCTTACCAAGCTCAATGCTTTTATGTATGTGCGC 1970
Db 1741 CCACTTACCAACCTGTGTGAAAGCTTACCAAGCTCAATGCTTTTATGTATGTGCGC 1800
Qy 1971 CCCCTCGCGCGCGAATTTTCTGCGCATGAGAGTGTGCTTACCTGTGTGACCCCA 2030
Db 1801 CCCCTCGCGCGCGAATTTTCTGCGCATGAGAGTGTGCTTACCTGTGTGACCCCA 1860
Qy 2031 AGTAGAGTTAGTGTGCGCTTGTGCGCTGCGCTGCGCGAGTACGATCTGTGACCTGA 2090
Db 1861 AGTAGAGTTAGTGTGCGCTTGTGCGCTGCGCTGCGCGAGTACGATCTGTGACCTGA 1920
Qy 2091 GAGTCTTGTGTAAACAGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 2139
Db 1921 GAGTCTTGTGTAAACAGACGAGTCAAAAAAAAAAAAAAAAAAAAAA 1969
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RESULT 10
US-10-627-886-7
; Sequence 7, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95

ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5880

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-627-886-7

Query Match 92.0%; Score 1969; DB 19; Length 1969;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 GCGTTAGCAGATCTTCAAGAACAGCTGACACACCTGCGCATTTGGCGGCGCAAGGC 480
651 GCGTCCGACTTTCGACCCCAAGAGGCGAGAGCGAGCGAGGTGATGCGCTTCTGCACTCC 710
481 GCGTCCGACTTTCGACCCCAAGAGGCGAGAGCGAGGTGATGCGCTTCTGCACTCC 540
711 TTCAATGACCGAGCTGACGCGGCACATAGCTAGCGAGAGCTGCGCCGCGCGACATC 770
541 TTCAATGACCGAGCTGACGCGGCACATAGCTAGCGAGAGCTGCGCCGCGCGACATC 600
771 GCGGTGGGCGCGCGCGAGATTGGCTACTTTTGGCGCAGTACCAAGGCGCATCACCAAGAC 830
601 GCGGTGGGCGCGCGCGAGATTGGCTACTTTTGGCGCAGTACCAAGGCGCATCACCAAGAC 660
831 TACACCGCGCTGCTGACCCCGAAGGCGCAGAGATATGCGGCTCCAGATCCGCGCCGAG 890
661 TACACCGCGCGTGTGACCCCGAAGGCGCAGAGATATGCGGCTCCAGATCCGCGCCGAG 720
891 GCCACCGGCTTACGCGCGCGCTGCTTTTGTGAGAACTGCTGAAGACCAAGGCGGAGAC 950
721 GCCACCGGCTTACGCGCGCGCTGCTTTTGTGAGAACTGCTGAAGACCAAGGCGGAGAC 780
951 CTCAGAGGCGAAGCGCTGCTGCTGCTGCGCGCGGCAACGTTGCGCCAGTCTGCGCGGAG 1010
781 CTCAGAGGCGAAGCGCTGCTGCTGCTGCGCGCGGCAACGTTGCGCCAGTCTGCGCGGAG 840
1011 CTGCTGCTGAGAGAGGCGCGCATCTGTCGTGCTGTCCTGCTCCAGGCTACGTTGATC 1070
841 CTGCTGCTGAGAGAGGCGCGCATCTGTCGTGCTGTCCTGCTCCAGGCTACGTTGATC 900
1071 GAGCCCAACGCGCTTACGCGCGGACAGCTGACGCGGTGCGAGCATGAAGAAAGAAAC 1130
901 GAGCCCAACGCGCTTACGCGCGGACAGCTGACGCGGTGCGAGCATGAAGAAAGAAAC 960
1131 AACAGCGCGCGCATCTCGAGTACCAAGAGGACACCGCGGTATGTAGGCGGACCGCGCG 1190
961 AACAGCGCGCGCATCTCGAGTACCAAGAGGACACCGCGGTATGTAGGCGGACCGCGCG 1020
1191 AAGCGTTGGAGGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGCGCACCAAGAGAG 1250
1021 AAGCGTTGGAGGCTGAGCTGCGAGGTGAGCATGCGCTTCCCTGCGCACCAAGAGAG 1080
1251 ATGATGAGCAGCAGCGCGGAGCTGCTGATCAAGCAGCGCTGCGCATGCTGTGTGAGAGGC 1310
1081 ATGATGAGCAGCAGCGCGGAGCTGCTGATCAAGCAGCGCTGCGCATGCTGTGTGAGAGGC 1140
1311 GCCAATGCGCTTCCACCAAGAGGCGCATCAAGATCAAGAGGCGCGGATCATCTTAC 1370
1141 GCCAATGCGCTTCCACCAAGAGGCGCATCAAGATCAAGAGGCGCGGATCATCTTAC 1200
1371 TGCCCCGCGAAGGCGGCGCAACGCGCGGCGCGTGGCGGTGACGCGCTGAGATGACCCAG 1430
1201 TGCCCCGCGAAGGCGGCGCAACGCGCGGCGCGTGGCGGTGACGCGCTGAGATGACCCAG 1260
1431 AACCGCATGAGCTGAACTGGAATCTCGGAGAGAGTTTGGCAAGAGCTGAGAGCGCATATG 1490
1261 AACCGCATGAGCTGAACTGGAATCTCGGAGAGAGTTTGGCAAGAGCTGAGAGCGCATATG 1320
1491 AAGGACATTCACGATCGGCGCATGAGGCGGCTCCGCGAGATACAAATGTTGACTTGGCTGGC 1550
1321 AAGGACATTCACGATCGGCGCATGAGGCGGCTCCGCGAGATACAAATGTTGACTTGGCTGGC 1380
1551 GCGCGCAACATCGCGGCTTACCAAGAGTGTGATGCGCTCAAGGCGCGGCGCTGT 1610
1381 GCGCGCAACATCGCGGCTTACCAAGAGTGTGATGCGCTCAAGGCGCGGCGCTGT 1440
1611 TAACTGCCAAGCGCGCAAGCGGCTACCGGCAATCAACCAACCAACTCAACGCGCC 1670

844 GTGGCCAGTACTGCGGAGCTGCTGTGAGAGAGGCGGCATGCTGTCTGCTGCTCC 903
1050 GACTCCAGGAGCTAGTGTAGAGAGCCCAAGGCTTCAAGCGAGAGCTGAGAGGAGT 1109
904 GACTCCAGGAGCTAGTGTAGAGAGCCCAAGGCTTCAAGCGAGAGCTGAGAGGAGT 963
1110 CAGGATGAG 1169
964 CAGGATGAG 1023
1170 GTGATGTGGGAG 1229
1024 GTGATGTGGGAG 1083
1230 CCGTCCGAG 1289
1084 CCGTCCGAG 1143
1290 TGCCAGTACGTGTGAG 1349
1144 TGCCAGTACGTGTGAG 1203
1350 AACAG 1409
1204 AACAG 1263
1410 AGCGAGCTGAG 1469
1264 AGCGAGCTGAG 1323
1470 GACAGAGCTGAG 1529
1224 GACAGAGCTGAG 1383
1330 TACAGAGCTGAG 1589
1384 TACAGAGCTGAG 1443
1590 GTCAAG 1649
1444 GTCAAG 1503
1650 AAC 1652
1504 AAC 1506

RESULT 12
US-10-627-886-23
Sequence 23, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UP-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1506 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1464
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-627-886-23
Query Match 70.2%; Score 1501.4; DB 19; Length 1506;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1502; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
150 AAGGCCCTCGCTGAGAGAGAGAGATCCCGCATGAGACGCCAACAACCGGAGATTGACG 209
4 ATGGCCCTTCGCTGAGAGAGAGAGATCTCGCATGAGACGCCAACAACCGGAGATTGACG 63
210 GCGCTGAG 269
64 GCGCTGAG 123
270 GGCATCAAGAACCCCGAGCGGCGGCGAGCTGACGAGATCTTCATGAGAGAGCGGAG 329
124 GGCATCAAGAACCCCGAGCGGCGGCGAGCTGACGAGATCTTCATGAGAGAGCGGAG 183
330 CAGCAGAGATTGAG 389
184 CAGCAGAGATTGAG 243
244 AAGGCCCGAGCTGCGCCATCTTCAACAGATCGTTGAGCGTGAAGCGGATCACC 303
450 TTCCGCTGCTGCTGAG 509
304 TTCCGCTGCTGCTGAG 363
510 CAGTACTGCTGCGCATCGGCGCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 569
364 CAGTACTGCTGCGCATCGGCGCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
570 CTGTCAATCAAG 629
424 CTGTCAATCAAG 483
630 CCGATGGGCGGCGAG 689
484 CCGATGGGCGGCGAG 543
690 GTGATGGCTTTCGAG 749
544 GTGATGGCTTTCGAG 603
750 GACGTGCCCGCGAG 809

Db 604 GACGTGCCCCGCGGACATCGGCGTGGCGCGCGAGATTGGTACTTTTGGCCAG 663
Qy 810 TACAAAGCCATCAACCAAGATCAACCGCGTGTCTGACCCCGAAGGCGCAGATATGCG 869
Db 664 TACAAAGCCATCAACCAAGATCAACCGCGTGTCTGACCCCGAAGGCGCAGATATGCG 723
Qy 870 GACCTCCGAGATCCGCGCGGAGCCGCGCTACCGGCGCGTGTCTTGTGGAGAACGTG 929
Db 724 GACCTCCGAGATCCGCGCGGAGCCGCGCTACCGGCGCGTGTCTTGTGGAGAACGTG 783
Qy 930 CTGAAGACCAAGGCGGAGAGCTCAAGGCGCAAGCGCTCTGTGTCTTGTGGCGCGCAAC 989
Db 784 CTGAAGACCAAGGCGGAGAGCTCAAGGCGCAAGCGCTCTGTGTCTTGTGGCGCGCAAC 843
Qy 990 GTGGCCCACTACTGCGCGGAGAGCTGTCTGTGAAGAGGCGCGCATGTCTGTCTGTC 1049
Db 844 GTGGCCCACTACTGCGCGGAGAGCTGTCTGTGAAGAGGCGCGCATGTCTGTCTGTC 903
Qy 1050 GACTCCCAAGGCTACGTGTAGAGCCCAAGCGCTTCAAGCGCGGAGAGCTGAGCGCGTG 1109
Db 904 GACTCCCAAGGCTACGTGTAGAGCCCAAGCGCTTCAAGCGCGGAGAGCTGAGCGCGTG 963
Qy 1110 CAGACATGAAGAAAGAAACAACAGCGCCCGCATCTCCAGTACAAAGAGCAACCGCC 1169
Db 964 CAGACATGAAGAAAGAAACAACAGCGCCCGCATCTCCAGTACAAAGAGCAACCGCC 1023
Qy 1170 GTGTATGTGGCGGACCGCGCAAGCTTGGAGAGCTGTGAAGAGGCGCGCATGTCTGTC 1229
Db 1024 GTGTATGTGGCGGACCGCGCAAGCTTGGAGAGCTGTGAAGAGGCGCGCATGTCTGTC 1083
Qy 1230 CCCTGCGCGCACCAAGAGATGATGAGACGAGCGCGCGCATGTCTGATGAAGAGCGCG 1289
Db 1084 CCCTGCGCGCACCAAGAGATGATGAGACGAGCGCGCGCATGTCTGATGAAGAGCGCG 1143
Qy 1290 TGCCAGTACTGTGTGAGAGGCGCCCAACATGCGCTTCAACAGAGCGCATCAAGATAC 1349
Db 1144 TGCCAGTACTGTGTGAGAGGCGCCCAACATGCGCTTCAACAGAGCGCATCAAGATAC 1203
Qy 1350 AACCAAGCGCGCATCTACTTGTCCCGGCAAGGCGCGCAACGCGCGCGCGTGTG 1409
Db 1204 AACCAAGCGCGCATCTACTTGTCCCGGCAAGGCGCGCAACGCGCGCGCGTGTG 1263
Qy 1410 AGCGGCGCGGAGATGACCCCAAGCGCATGAGCGCGCAACGCGCGCGCGTGTG 1469
Db 1264 AGCGGCGCGGAGATGACCCCAAGCGCATGAGCGCGCAACGCGCGCGCGTGTG 1323
Qy 1470 GACAAGCTGAGCGCATCATGAAGACATCTACGACTCCGCAATGAGGCGTCCGCA 1529
Db 1324 GACAAGCTGAGCGCATCATGAAGACATCTACGACTCCGCAATGAGGCGTCCGCA 1383
Qy 1530 TACAATGTTGACTGTGCGCGCGCGCAACATCGCGGCGCTTACCAAGTGTGATGCC 1589
Db 1384 TACAATGTTGACTGTGCGCGCGCGCAACATCGCGGCGCTTACCAAGTGTGATGCC 1443
Qy 1590 GTCAAGGCGCGGCGCGCTGTTAAGCTGCCAAGGCGCGCAAGCGCGCTCACCGCAATCC 1649
Db 1444 GTCAAGGCGCGGCGCGCTGTTAAGCTGCCAAGGCGCGCAAGCGCGCTCACCGCAATCC 1503
Qy 1650 AAC 1652
Db 1504 AAC 1506

RESULT 13
US-09-070-844-25
Sequence 25, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

Qy 183 ATGAGCGCACACCGCGGACTTCAAGCGCGTGTGAAGAGCGGATGCGCAC 242
Db 4 ATGAGCGCACACCGCGGACTTCAAGCGCGTGTGAAGAGCGGATGCGCAC 63
Qy 243 AAGCGGCGCACTGAGGCGCTGTGTGACAGGATCAAGAACCCCGAGTGTGCGTGTG 302
Db 64 AAGCGGCGCACTGAGGCGCTGTGTGACAGGATCAAGAACCCCGAGTGTGCGTGTG 123
Qy 303 ACCGAGATCTTCAAGAGACCCGAGACAGAGGATTCATGACAGCGGTGCGAGGTG 362
Db 124 ACCGAGATCTTCAAGAGACCCGAGACAGAGGATTCATGACAGCGGTGCGAGGTG 183
Qy 363 GCGGTCTCCCTGACGCGCGTGTGTGAGAGGCGCGGAGTGTGCGCATCTTCAAGCAG 422
Db 184 GCGGTCTCCCTGACGCGCGTGTGTGAGAGGCGCGGAGTGTGCGCATCTTCAAGCAG 243
Qy 423 ATCGTTAGCTGAGCGCGGTGATCACTTCCGCGTGTGTGAGAGCGCGGCAAC 482
Db 244 ATCGTTAGCTGAGCGCGGTGATCACTTCCGCGTGTGTGAGAGCGCGGCAAC 303
Qy 483 CTGAGGTCAACCGCGCTTCCGCGTGTGAGTACTGTGCGCATGCGCGCTTCAAGGCG 542
Db 304 CTGAGGTCAACCGCGCTTCCGCGTGTGAGTACTGTGCGCATGCGCGCTTCAAGGCG 363
Qy 543 GCGGTGCGTTCACCGCTTCCGCGTGTGAGTACTGTGCGCATGCGCGCTTCAAGGCG 602
Db 364 GCGGTGCGTTCACCGCTTCCGCGTGTGAGTACTGTGCGCATGCGCGCTTCAAGGCG 423
Qy 603 ATCTTAAGAAACGCGTGAACCGCTGTGCGCATGAGGCGCGGCGCGTGTGCGACTTC 662

Query Match 68.7%; Score 1470; DB 9; Length 1473;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-070-844-25

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WhiteLock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1431

Db	424	ATCTTCAGGAACAGCCTGACCACTTGCCTCATGGCGGCGCAAGGGCGCTCCGACTTC	483
QY	663	GACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCGAGTCTTCAATGACCGAG	722
Db	484	GACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCGAGTCTTCAATGACCGAG	543
QY	723	CTGCAAGCGCCACATCAGCTACGTGAGAGACGTGCCCGCGCGGACATATGGGCTGGGCGCG	782
Db	544	CTGCAAGCGCCACATCAGCTACGTGAGAGACGTGCCCGCGCGGAGATGCGCTGGGCGCG	603
QY	783	CGCGAGATTGGCTACTTTTCGGCCAGTACCAAGCCCATCAACCAAGACTACCGGCGTG	842
Db	604	CGCGAGATTGGCTACTTTTCGGCCAGTACCAAGCCCATCAACCAAGACTACCGGCGTG	663
QY	843	CTGACCCCGAAGGGCCAGAGATGAGCGGCTTCCGAGATCCGCCCCAGAGCCACCGGCTAC	902
Db	664	CTGACCCCGAAGGGCCAGAGATGAGCGGCTTCCGAGATCCGCCCCAGAGCCACCGGCTAC	723
QY	903	GGCGCCGTGCTTTTGTGTGAGAACCTGCTGAAGAGCAAGGGCGAGAGGCTTCAAGGGCAAG	962
Db	724	GGCGCCGTGCTTTTGTGTGAGAACCTGCTGAAGAGCAAGGGCGAGAGGCTTCAAGGGCAAG	783
QY	963	CGCTGCTGTGTCTGCGCGGGGCAACGTGGGCCAGTACTGGCGCGGACCTGCTGTGGAG	1022
Db	784	CGCTGCTGTGTCTGCGCGGGGCAACGTGGGCCAGTACTGGCGGAGCTGCTGTGGAG	843
QY	1023	AAGGGCGCATCGTGTGTGTGTGCGTGTCCGACTTCCAGGGCTACGTGTACGAGCCCAAGGAC	1082
Db	844	AAGGGCGCATCGTGTGTGTGTGCGTGTCCGACTTCCAGGGCTACGTGTACGAGCCCAAGGAC	903
QY	1083	TTTCACGCGCGGACAGCTCAGCGCGGTGTGAGGACATGAAGAGAAAGAAACAACAGCGCCCGC	1144
Db	904	TTTCACGCGCGGACAGCTCAGCGCGGTGTGAGGACATGAAGAGAAAGAAACAACAGCGCCCGC	963
QY	1143	ATTCTCCAGTACCAAGAGGCAACACCGCTGTATGTGGCGGACCGCGCAAGGCTTGGGAG	1202
Db	964	ATTCTCCAGTACCAAGAGGCAACACCGCTGTATGTGGCGGACCGCGCAAGGCTTGGGAG	1022
QY	1203	CTGCACTGCCAGTGGACATCGCTTCCCTTCGCGCATCCAGACCAGAACGAGATCGATGAGCAC	1262
Db	1024	CTGCACTGCCAGTGGACATCGCTTCCCTTCGCGCATCCAGAACGAGATCGATGAGCAC	1083
QY	1263	GACGCGGAGCTGTGATGTAAGAAGGCGTGCAGATGATGTGTGAGAGGGGCGCAACATGGCCC	1322
Db	1084	GACGCGGAGCTGTGATGTAAGAAGGCGTGCAGATGATGTGTGAGAGGGGCGCAACATGGCCC	1144
QY	1323	TTCACCAACGAGGCCATCCACAAATGTAACAAGGCGCGCATCATCTACTGCCCGGCAAG	1382
Db	1144	TTCACCAACGAGGCCATCCACAAATGTAACAAGGCGCGCATCATCTACTGCCCGGCAAG	1202
QY	1383	GCGGCGAACGCGCGCGGTGGCGGTCAAGCGGCTCTGAGATGACCCAGAACCGCATGAGC	1442
Db	1204	GCGGCGAACGCGCGCGGTGGCGGTCTAAGCGGCTCTGAGATGACCCAGAACCGCATGAGC	1263
QY	1443	CTGAACCTGGAATCCGAGAGAGTTTGGCACAACGCTGGAGCGCATATGATGAAGACATCTAC	1502
Db	1264	CTGAACCTGGAATCCGAGAGAGTTTGGCACAACGCTGGAGCGCATATGATGAAGACATCTAC	1322
QY	1503	GACTCCGCAATGGGGCGTCCCGCAGATACAAATGTTGAATCTGGCTGCGGGCGCCCAACATC	1562
Db	1324	GACTCCGCAATGGGGCGTCCCGCAGATACAAATGTTGAATCTGGCTGCGGGCGCCCAACATC	1383
QY	1563	GCGGGCTTACCAAGGTGGCTGTATGCGGTCAAGGCCCAAGGGCGCTGTTAAGCTGCCAG	1622
Db	1384	GCGGGCTTACCAAGGTGGCTGTATGCGGTCAAGGCCCAAGGGCGCTGTTAAGCTGCCAG	1443
QY	1623	GCCCAAGCCAGGCTCAACCGGTAATCCAAC	1652
Db	1444	GCCCAAGCCAGGCTCAACCGGTAATCCAAC	1473

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US-10-627-886-25
; Sequence 25, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE -- AND --SUBUNITS OF GLUTAMATE
; DEHYDROGENASES AND METHODS OF USE
;
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606-6669
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,886
; FILING DATE: 24-Jul-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,844
; FILING DATE: 01-MAY-98
; APPLICATION NUMBER: 08/725,596
; FILING DATE: 03-OCT-96
; APPLICATION NUMBER: 08/541,033
; FILING DATE: 06-OCT-95
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: UF-155CD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5600
;
; INFORMATION FOR SEQ ID NO: 25:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4..1431
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-627-886-25
Query Match 68.7%; Score 1470; DB 19; Length 1473;
Best Local Similarity 100.0%; Pident. No. 0;
Matches 1470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 183 ATGACGCCACACCAGCGGACATTTCACGCGCGTTCGAGAAAGCGGGTGAACACAGATGSCCAC 242
Db 4 ATGACGCCACACCAGCGGACATTTCACGCGCGTTCGAGAAAGCGGGTGAACACAGATGSCCAC 63
QY 243 AAGCGGGGCACTGAGAGGCGCTGTGTCAACGCGCATCAAGAACCCCGACGTCGCGCAGCTGTG 302
Db 64 AAGCGGGGCACTGAGAGGCGCTGTGTCAACGCGCATCAAGAACCCCGACGTCGCGCAGCTGTG 123
QY 303 ACCGAGATCTTCATGAAGAGACCCGAGACGAGAGATTTCATGACAGCGGTGCGCGAGGTG 362
Db 124 ACCGAGATCTTCATGAAGAGACCCGAGACGAGAGATTTCATGACAGCGGTGCGCGAGGTG 183
QY 363 GCCGTCTCCCTGCAAGCCCGTGTGTGAGAAAGCCCCCAGCTGCTGCCATCTTCAAGAG 422
Db 184 GCCGTCTCCCTGCAAGCCCGTGTGTGAGAAAGCCCCCAGCTGCTGCCATCTTCAAGAG 243

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Qy 435 GAGCGCTGATACCTTCCGGTGTCTGGCTGAGACGCGGCAACTGCAAGTCAAC 494
Db 166 GAGGGGGGAGATCCGTGTTCCGGTACCTTGGGTCAACACAGGCGCGGGTACCGGTCAAC 225
Qy 495 GCGGCTTCCGGCTGAGTACTGTCGCCATCGGCCCTTACAAAGGCGGCTGCGCTTC 554
Db 226 CGTGGCTACCGGGGAGATGACGAGCGCCATCGGCCCTTACAAAGGCGGCTGCGCTTC 285
Qy 555 CAGCCCTCCGGAACCTGTCCATCATGAGTTCCTTGGGAGGATCTTCAAGAC 614
Db 286 CATCTCTGGCAACTCGGGGGTCTGAAGTTCCTCGCTTCAAGAGTCTTCAAGAAC 345
Qy 615 AGCTTGACCAACCTTGCCCATGAGCGGCGCAAGGCGGCTTCCGACTTCAACCCCAAGGC 674
Db 346 TCCCTGACCACTCTGCCCATGAGGCGGCGCAAGGCGGCTTCCGACTTCAACCCCAAGGC 405
Qy 675 AAGAGCGACCGGAGGATGATGCGCTTCTGCCAGTCTTCAATGACCGAGCTGACGCGCAC 734
Db 406 AAGAGCGACCGGAGGATGATGCGCTTCTGCCAGTCTTCAATGACCGAGCTGATCCGCAC 465
Qy 735 ATGAGCTACGTCGAGGAGCGTCCCGCGGCGCAATCGGCGTGGGGCGGCGGAGATGGC 794
Db 466 GTGCGGCGCGACCTGACGTCGCGCGCGCAATCGGCGTGGCGCGGAGATCGGC 525
Qy 795 TACCTTTTCCGCGCAGTACCAAGCGCATCACCAAGAACTACACCGGCGTGTGACCCCGAAG 854
Db 526 TACCTGTTCCGCGCAGTACCAAGCGCCTGTCCACCAAGTTCACTGCGTGTGACCCCGAAG 585
Qy 855 GCGCGAGAGTATGGCGGCTCCGAGATCGGCCCGAGCGCACCGGCTACCGGCGCTGTCTG 914
Db 586 GCGCTGAGCTATGGCGGCGAGCTGATCGGCCCGAGGCGACCGGCTTCCGCTGCTTAC 645
Qy 915 TTTGTGAGAACGTCGTGAAGGACCAAGGGGAGAGCCTCAAGGGGAGCGCTGCTGTG 974
Db 646 TTTGCCCAAGAAATGCTCAAGAGATCGTGGCGGCGCTTCAAGGCGAGCGGAGTGCATC 705
Qy 975 TCTGGCGCGGCAACGTGCGCCAGTACTGCGCGAGGCTGTGTGAGAAAGGCGGCATC 1034
Db 706 TCCGCGCTCGGCGCAACGTGCGCCAGTACGCGGCGCGCAAGGTCAATGAAATGGGCGGCAAG 765
Qy 1035 GTGCTGTGCTGTCTCGAATCCCAAGGCTACGTTACGAGCCCAACGCGCTTCAAGCGGAG 1094
Db 766 GTGATCTCGCTGTCTCGAATCCCAAGGCACTGTATGCTCGAGCGGCGCTTCCGAGAG 825
Qy 1095 CAGCTGAGGCGGTGAGGAGATGAGAAAGAAACAACGCGGCCGATCTCCGAGTAC 1154
Db 826 CAGTGGGAATACGTGATGAGCTGAAGAACGTG--CGCGCGGGCGCATCTCGGAGATG 882
Qy 1155 AAGAGCGACACCGCGGTATGTGGGCAACCGCGCAAGCCTTGTGAGCTGAGCTGCAG 1214
Db 883 GCGGAGCAGTTTTCCTGCAATTTCTGAAAGGCGCGGCGCTGGGCTGTGGCTGC--- 939
Qy 1215 GTGAGCATCGCTTTCCTGCGGCAACCCCAAGACGAGATCGATGACGAGCGGAGCTG 1274
Db 940 ---GATATCGGCTGCGCTTGGCGCAACCGAACTGATGCCGAGATGCGCGGCGC 996
Qy 1275 CTGATCAAGCACGCGCTGCAATGATGAGGAGGCGCAACATGCCCTCAACCAAGAG 1334
Db 997 CTGCTGGCCAAAGGCTGTGTGTGCGCGAAAGGCGCAACATGCCCTCAACCTGAAA 1056
Qy 1335 GCCATCCACAAGTACAAACAAGGCGGCACTCATCTGCCCCGAGCAAGGCGGCAAGCGC 1394
Db 1057 GCGGTGACCTGTTCCTGAGGCGGCACTCTACCGCGCGGCAAGGCGGTGAGACGCC 1116
Qy 1395 GCGGCGTGGCGGTCAAGGCGCTTGAAGATGACCAAGAACCGCATGAGCTGAACTGACT 1454
Db 1117 GCGCGGCTGGCGGTGAGCGGCGCTGAGATGTGCAAGAACCGCATGCGCTGTGGAGC 1176
Qy 1455 CGGAGGAGGTTCGCGCAAGGCTGAGCGCATCATGAAAGACATCTAGCATCTCGGCATG 1514
Db 1177 GAGGGCGAGGTGATACCAAGCTGACGCGCATCATGAGTCACCAATGCTGCTGCTG 1236

Qy 1515 GAGCGCTCCGAGATA---CAATGTTGACTTGGCTGCGGCGCCCAACATCGGCGGCTTC 1571
Db 1237 CTGTACGGCGAGAGAGAGAGGCGGCGGTCACTACGTAAAGGGGCGAAACATCGCGGCTTC 1296
Qy 1572 ACCAAGTGTGATGCTGCTCAAGGCGCCAGAGGCGCTGTTAA 1613
Db 1297 GTCAAGTGTGCGATGCGATGCTGCGCGAGGCGGTGTCTGA 1338

Search completed: July 10, 2005, 00:07:50
Job time : 1216 secs

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2	385	18.7	9123	8	BZ569676	BZ569676	pac92-164
3	358.2	16.0	9232	8	BZ578032	BZ578032	msh2-56878
4	350.2	16.4	8988	7	CV2119575	CV2119575	EST8792857
5	333.6	15.1	7787	7	CV2111069	CV211069	EST8707797
6	305.6	14.3	1114	9	CNS0600N	1411141	T3 end c6
7	282.4	13.7	854	5	BM480553	BM480553	BM480553
8	288.6	13.5	943	7	CV211068	CV211068	EST870778
9	282.8	13.2	540	1	AU186881	AU186881	AU186881
10	281	13.1	820	9	CL693787	CL693787	PR10162C
11	274.6	12.8	6787	7	CF839691	CF839891	pABH004KXF
12	271.6	12.7	737	5	BM436105	BM436105	BM436105
13	270	12.6	694	5	BM438709	BM438709	BM438709
14	269	12.6	730	5	BM475527	BM475527	BM475527
15	266	12.4	527	1	AU196696	AU196696	AU196696
16	264.4	12.4	790	7	CF693244	CF693244	CCAHU32TR
17	263.4	12.3	835	7	CF709188	CF709188	CCADBS6TR
18	263.4	12.3	836	7	CF71421	CF71421	CCAD746TR
19	262.8	12.3	811	7	CF701425	CF701425	CCAHN84TR
20	262.8	12.3	815	7	CF678148	CF678148	CCAH141TR
21	262.8	12.3	817	7	CF715582	CF715582	CCAP145TR
22	262.8	12.3	820	7	CF676255	CF676255	CCAHK59TR
23	262.8	12.3	826	7	CF687048	CF687048	CCAD07TR
24	262.8	12.3	826	7	CF711744	CF711744	CCAGK82TR

25	262.8	12.3	83.6	7	CF659575	CF659433R
26	262.8	12.3	862.7	1	CF662961	CCAM409R
27	262.8	12.3	837	7	CF679076	CCAF9687R
28	262.8	12.3	837	7	CF654808	CF659488R
29	262.8	12.3	837	7	CF705643	CCAD537TR
30	262.8	12.3	838	7	CF715667	CF705643
31	262.8	12.3	845	7	CF699111	CCAB826TR
32	262.8	12.3	845	7	CF706882	CCAGV01TR
33	262.8	12.3	845	7	CF706882	CCAH016TR
34	262.8	12.3	847	7	CF690384	CCACG34TR
35	262.8	12.3	848	7	CF707240	CCAG192TR
36	262.8	12.3	853	7	CF718447	CCADB79TR
37	262.8	12.3	859	7	CF708923	CCAA257TR
38	262.8	12.3	860	7	CF657244	CCAH824TR
39	262.8	12.3	860	7	CF690169	CCAC352TR
40	262.8	12.3	863	7	CF722210	CCAD003TR
41	262.8	12.3	865	7	CF682477	CCAE155TR
42	262.8	12.3	869	7	CF720318	CCABP77TR
43	262.8	12.3	870	7	CF694123	CCAI662TR
44	262.8	12.3	874	7	CF706705	CCAD272TR
45	262.8	12.3	885	7	CF663316	CF693316
			890	7	CF693859	CCAO016TR

ALIGNMENTS

	RESULT	1		
	BZ569675			
	LOCUS	BZ569675	1245 bp	DNA Linear GSS 17-DEC-2002
	DEFINITION	pacs2-164_965.g1 pacs2-164 Pseudomonas aeruginosa genomic clone		
	ACCESSION	BZ569675		
	VERSION	BZ569675.1	GI:27204622	
	KEYWORDS	GSS.		
	SOURCE	Pseudomonas aeruginosa		
	ORGANISM	Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. 1 (bases 1 to 1245) Spencer,D.H., Raymond,C.K., Smith,B.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library J. Bacteriol. (2002) In press Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954 Fax: 2066857244 Email: craymond@u.washington.edu Class: Shotgun.		
	JOURNAL COMMENT	Location/Qualifiers		
	FEATURES	source		
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	/strain="2-164"			
	/db_xref="taxon:287"			
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	/clone_id="pacs2-164"			
	/note="clinical isolate 2-164 Whole genomic shotgun library."			
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	Best Local Similarity	74.2%; Pred. No. 1,4e-68;		
Matches	500; Conservative	0; Mismatches 174;	Indels	0; Gaps 0;
OY	450	TTCGCGTGTCCGGCTGAAGCAAGCAGCGGCACAATCGTAGGTCACACGCCGGCTTGCGGCTG	509	
	29	TTCGCGGTACCCTTGAGCTGACAGACAGAGCGCGGTACGAGTCAACTGAGCTACCGGAGTG	88	
OY	510	CAGTACTGTTCGCGCATCGGCCCTTACAGAAGGCGCGCTGCGCTTTCAACCCCTCCGTGAAC	569	

Db 89 CAGATGAGCAGCGCCATCGGCTCCCTTACAGGGCGGCTCGCTTCACTCCTCGGTCAAC 148

QY 570 CTGTTCATCATGAAGTTCTTGGCTTTGAGCAGATCTTCAAGAACAGCTGACCACTCTG 629

Db 149 CTCGGGGGTGCTGAAGTTCTCTCGCTTCCAGCAGAGCTTCAAGAACTCCCTGACCACTGTG 208

QY 630 CCCATGGGCGCGCGCAAGGGGCGGCTCCGACTTTCGACCCCAAGGGCAAGGGAAGCGCGAG 689

Db 209 CCCATGGGCGCGCGCAAGGGCGGCTCCGACTTTCGATCCGAAGGGCAAGGGAAGCGCGAG 268

QY 690 GTGATGCGCTTCTGCGAGTCTCTTACAGCCGAGCTGCAGCGCCACATCAGCTACGTGCAG 749

Db 269 GTGATGCGCTTCTGCGAGTCTCTTACAGCAGAGCTGTACCCGCCACGTGCGCGCGACTTG 328

QY 750 GACGTGCGCGCGCGGAGCATGCGGGTGGGGCCCGCGAGATTGGCTACTCTTTTGGCGCAG 809

Db 329 GACGTGCGCGCGCGGAGCATGCGGCTCGGCGCGCTGAGATCGGCTTACTCTGTTGCGGCGAG 388

QY 810 TACAAGCGCATCACCCAGAACTACAACCGGCGTGTCAACCCCGAAAGGCGCAGAGATATGGC 869

Db 389 TACAAGCGCCTGTGCCAACAGTCTCACTCGGTGCTGACCGGCAAGGGCGCTGAGCTATGGC 448

QY 870 GGGCTCCGAGATCCCGCCCGGAGCCACCGGCGCTACCGGCGCGCTGTCTTTGTGAGAACTGT 929

Db 449 GGGAGCATGATTCGCGCCGAGGCGACCGGCTTCGCTCGCTACTTGGCCCAAGGAATG 508

QY 930 CTGAAGGCAAGGGCGAGAGGCTCTCAAGGGCAAGCGCTTCTGTGTCTTGCGCGCGGCAAC 989

Db 509 CTCAAGAGATCGTGGCGCGGCTTGACGGCCAGCGGGGTGGCGATCTCCGGCTCGGGCAAC 568

QY 990 GTGGCCCAAGTACTGCGCGGAGCTGTGTGAGAAAGGGCGGCATCTGTCTGTCTGCTGTC 1049

Db 569 GTGCGCCAGTACGGGCGCGCAAGGTCAATGAAATGGCGGCAAGTATCTCGCTGTC 628

QY 1050 GACTTCCAGGCGCTACGTGTACGAGCCCAAGGCTTCAAGCGCGAGCAGACTGACGCGGTG 1109

Db 629 GATTCCGAAGTCACTCTGTATGCGAGGCGGGGCTCTTCGACGAGCAGTGGGAATACCTG 688

QY 1110 CAGGACATGAAGAA 1123

Db 689 AATGAGCTTAAAGAA 702

RESULT 2	
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LOCUS	1123 bp DNA linear GSS 17-DEC-2002
DEFINITION	pacs2-164_965.s2 pacs2-164 <i>Pseudomonas aeruginosa</i> genomic clone
ACCESSION	pacs2-164_965, genomic survey sequence.
VERSION	BZ569676
KEYWORDS	BZ569676.1 GI:27204626
SOURCE	GSS.
ORGANISM	<i>Pseudomonas aeruginosa</i> <i>Pseudomonas aeruginosa</i> Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; <i>Pseudomonadaceae</i> ; <i>Pseudomonas</i> . 1 (bases 1 to 1123) Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isolates of <i>Pseudomonas aeruginosa</i> library <i>J. Bacteriol.</i> (2002) In press Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062316954 Fax: 2066857244 Email: craymond@u.washington.edu Class: shotgun.
TITLE	
JOURNAL	
COMMENT	
FEATURES	
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Best Local Similarity	72.8%;	Pred. No. 1.8e-66;		
Matches 496;	Conservative 0;	Mismatches 185;	Indels 0;	Gaps 0;

OY	450	TTCCGCGGTGCTCTGGCTGGAGCAAGCCGGGCAACCTCGAGGTCAACCGCGGCTTCCGGCTG	509
Db	38	TTCCGCGGTACCTTGGGTGACGACACAGGCCCGGGTACGGGTCAACCTGGCTACCGGGTG	97
OY	510	CAGTACTCTGTCCGCGCATCGGCCCCCTACAGAGCGCGGCTGCGCTTCAACCCCTCCGTGAAC	569
Db	98	CAGATGAGCAGACGGCGCATCGGCGCCCTTACAGAGGCGGGCTGCGCTTCCATCTCCCTCGGTCAAC	157
OY	570	CTGTCCATCANTGAAGTTCCTTGCTCGCTTGGAGAGATCTTCAAGAACCACTGACCAACCTG	629
Db	158	CTCGGGGTGTGAAAGTTCCTGCGCTTGGAGAGGTCTTCAAGAACTCCCTGACCACTCTG	217
OY	630	CCCATGGGCGCGGCGCAAGGCGGCTCCGACTTTCGACCCCAAGGGCGAAGCGACGCGGAG	689
Db	218	CCCATGGGCGCGGCGCAAGGCGGCTCCGACTTTCGATCCGAAGGGCGAAGCGACGCGGAG	277
OY	690	GTCATGGCGTCTTCCGACGTCTCTTATATACCGAGCTGAGGCGCCATCATCACTACGTAGCAG	749
Db	278	GTCATGGGTCTTCCGACGTCTCTTATATAGGAGCTGTACCGCACGTCGGCGCGCACCTG	337
OY	750	GACCTGCCCCCGGCGCATCTCGGCGTGGGCGCGCGCGCAGATTGGACTCTTTTCGCGCAG	809
Db	338	GACCTGCCCCCGGCGCATCTCGGCGTGGGCGCGCGGTGAGATCGGCTACCTGTTCCGCGCAG	397
OY	810	TACAAAGCGCATCAACCAAGAACTACACCGGCGGTCTGAACCCCGAAAGGCGCAGAGTATGGC	869
Db	398	TACAAAGCGCTGTTCACACAGTTTCACTCCGTGTGACCGGCAAGGGCGCTGAGCTATGGC	457
OY	870	GGCTCCGAGATTCGCGCCCCCGGACCGGCGTACCGCGCGCGTGTGTGTGAGAACTGTG	929
Db	458	GGCGACATGATTCGCGCCCCCGGAGGCGACCGGCTTCCGCTGTCTTACCTTCCCGCAGGAATG	517
OY	930	CTGAAGGACAAAGGCGAGAGCTTCAAGGGGCAAGCGCTGCTGTGTGTGCGCGGCGCAAC	989
Db	518	CTCAAGAGTCTGTGGCCCGCGCTTTCGACGGCCAGCGGCGGTGCGATCTCCGCGCTCGGCGCAAC	577
OY	990	GTCGCCCAAGTACCTGCGGAGCGCTGCTCTGTGAGAAAGGCGCCCATCTGCTGCTGCTGCC	1049
Db	578	GTCGCCCAAGTACCTGCGGCGCGCAGAGTATGAGAAATGGGCGGCAAGTGAATCTCCCTGTCC	637
OY	1050	GACTCCCAAGGCTTACGTGTACGAGCCCAACCGGCTTTCAGCGCGGACGACTGCAAGCGGATG	1109
Db	638	GATTCCGAAGGCAACCATGTATGTCGGAAGCGGGGCTCTCCGAACGACGAGTGGGGAATA	697
OY	1110	CAGGACATGAAGAAGAAAC 1130	
Db	698	ACTGAATGAGCTGAAGAAGAC 718	

RESULT 3				
LOCUS	BZ578032			
DEFINITION	BZ578032 922 bp DNA linear GSS 17-DEC-2002 msl2_5687.y2 msh Pseudomonas aeruginosa genomic clone msh2_5687, genomic survey sequence.			
ACCESSION	BZ578032			
VERSION	BZ578032.1	GI:27213093		
KEYWORDS	GSS.			
SOURCE	Pseudomonas aeruginosa			
ORGANISM	Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			

QY 621 ACCACCTGCCCATTGGGCGGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGAAGGC 680
Db 358 ACAACACTCCCAATGGGATGGGCGAAGGATGGTTCCGATTTTCAGCCAGCGGCAAGTCT 417
QY 681 GACCGGAGGTGATGCGCTTTCGCACTCTTCATGACCGAGCTGCAGCGCCACATCAGC 740
Db 418 GATGGCCAAAGTCAAGATTCCTGCGAGCTTCATGCTCGAACTTCAGCGCCACATCGGC 477
QY 741 TAGTGAAGAGCGCGCCGCGGAGACATGGCGGTGGGCGCGCGAGATTGGCTACTCT 800
Db 478 GCGAACACAGATGTCCTCAAGCTGTGATTCGATTCGATGCTCGTAAATCGCTACATG 537
QY 801 TTCGGCCAGTACAGCCCATCACCAAGAACTACACCGCGCTGCAGACCCCAAGGCGCAG 860
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QY 861 GAGTATGCGCGCTCCGAGATCCGCCGAGGCAACCGGCTACGCGCGCGCTGCTTTGTC 920
Db 598 CCATACCGTGGCTCACTGATCCGTCAGAAAGCTACAGGCTACGCTTCTTCTACTCTGTC 657
QY 921 GAGAACGCTGAGAGCAAGAGGCGAGAGCCTCAAGGCGCAAGCGCTGCTGCTGCTGCGC 980
Db 658 ACAGAAATGCTCCGTGCTAAGGCGAAGAGATCAAGGCGCAAGCGCTGCTGCTGCTGCGC 717
QY 981 GCGGCGCAAGCTGGCCCACTACTGCGCGAGCTGCTGCTGAGAAAGGCGCCATGCTGCTG 1040
Db 718 TCCGCGCAAGCTGGCCCACTACTGCGCGAGAGCTCAAGAGCTGCGGCGCAATCCGATC 777
QY 1041 TCGCTGTCCAGCTCCAGAGGCTACGTTGACGAGCCCAAGCGCTTCAAGCGCGAGCAGCTG 1100
Db 778 TCATGCTCAGACTCACAAGCGGCTCTCATCTTCAGGATGATGACAAAGAGACATCTT 837
QY 1101 CAGGCGGTGAGAGCATGAAGAA 1123
Db 838 GATGCTGTCATGCATCAAGAA 860

RESULT 5 778 bp mRNA linear EST 16-SEP-2004
CV211069
LOCUS EST870779 non-normalized T1 cDNA library Trichomonas vaginalis cDNA
DEFINITION
CV211069
VERSION CV211069.1 GI:52158049
KEYWORDS EST.
SOURCE Trichomonas vaginalis
ORGANISM Trichomonas vaginalis
REFERENCE Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
AUTHORS Trichomonadidae; Trichomonadinae; Trichomonas.
TITLE 1 (bases 1 to 778)
Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M.
The complete genome sequence of the sexually transmitted parasite
Trichomonas vaginalis
JOURNAL Unpublished (2004)
COMMENT Other ESTs: EST870778
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-9319
Fax: 301-838-0208
Email: carlton@igr.org
Seq primer: lambda Triplex2.
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SfiB; T. vaginalis strain T1 library constructed from
cDNA, made in lambda Triplex2. Inserts cloned
unidirectionally in the SfiA and SfiB sites. Mass excision
of library produced inserts in pTriplex2 plasmid. Inserts
sequenced from both 5' and 3' ends using Triplex2
sequencing primer and polydT 24 bp primer respectively."

ORIGIN
Query Match 15.1%; Score 323.6; DB 7; Length 778;
Best Local Similarity 65.8%; Pred. No. 3.3e-54;
Matches 470; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

QY 321 GACCGGAGCAGAGAGTTCATGACGCGCGCGGAGGTCGCTTCCTGACGCC 380
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QY 381 GTGTTGAGAGAGCGCCCGAGCTGCTGCCATCTTCAAGCATTCGTTGAGCTGAGCCG 440
Db 118 ATCTCGAAGAGAACCAAGTACAGAAAGCTCTCCAGCTCTTGTGAGCCAGAGCGT 177
QY 441 GTGATCACTTCGCGGTGCTGCTGAGACAGCGCGCAACCTGACAGTCAACGCGCG 500
Db 178 GTTATCATGTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
QY 501 TTCGCGTGCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 560
Db 238 TTCGCGTGCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 297
QY 561 TCCGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
Db 298 AACGTTAACTTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTC 357
QY 621 ACCACCTGCCCATTGGGCGGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGAAGAGC 680
Db 358 ACAACACTCCCAATGGGATGGGCGAAGGATGGTTCCGATTTTCAGCCAGCGGCAAGAGT 417
QY 681 GACCGGAGGTGATGCGCTTTCGCACTCTTCATGACGAGCTGCAGCGCCACATCAGC 740
Db 418 GATGGCCAAAGTCAAGATTCCTGCGAGTCTTATGCTCGAACTTTCAGCGCCACATCGGC 477
QY 741 TAGTGAAGAGCGTCCCGCGCGGAGACATGGCGGTGGCGCGCGAGATTGGCTACTCT 800
Db 478 GCGAACCAATATTCACAGAGGTGATGCGGTGGCTGCTGTAATTCGCTCAATG 537
QY 801 TTCGGCCAGTACAGCCCATCACCAAGAACTACACCGCGCTGCAGACCCCAAGGCGCAG 860
Db 538 TTCGGCCAGTACAGCCCATCACCAAGAACTACACCGCGCTGCAGACCCCAAGGCGCAGC 597
QY 861 GAGTATGCGCGCTCCGAGATCCGCCGAGGCAACCGGCTACGCGCGCGCTGCTTTGTC 920
Db 598 TCATGCGTGGCTCACTGATCCGTCAGAAAGCTACAGGCTACGCTTGTCTACTCTGTC 657
QY 921 GAGAACGCTGTAAGAGCAAGGCGGAGAGCTTCAAGGCGCAAGCGCTGCTGCTGCTG 980
Db 658 ACAGAAATGCTCCGTACTAAGGCGGAGAGATCAAGGCGCAAGCGCTGCTGCTGCTG 717
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RESULT 6 1114 bp DNA linear GSS 05-JUL-2001
CNS060UN
LOCUS T3 end of clone AN00A009C04 of library AN00A from strain CLIB 89 of
DEFINITION Yarrowia lipolytica, genomic survey sequence.
CV211141
VERSION AL411141.1 GI:12180271
KEYWORDS GSS.
SOURCE Yarrowia lipolytica
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.

REFERENCE 1 (bases 1 to 1114)
 AUTHORS Souciat,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 Boloitiin-Rukhara,M., Bon,E., Brottier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
 Malpety,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
 Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weisenbach,J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 11152876
 REFERENCE 2 (bases 1 to 1114)
 AUTHORS Casaregola,S., Neuvéglise,C., Lepingle,A., Bon,E., Feynerol,C.,
 Artiguenave,F., Wincker,P. and Galliardin,C.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
 lipolytica
 JOURNAL FEBS Lett. 487 (1), 95-100 (2000)
 MEDLINE 20584727
 PUBMED 11152892
 REFERENCE 3 (bases 1 to 1114)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,
 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
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 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.
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 similar to Saccharomyces cerevisiae ORF YOR375c [GDH1 ;
 glutamate dehydrogenase (NADP+)]"
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ORIGIN
 Query Match 14.3%; Score 305.6; DB 9; Length 1114;
 Best Local Similarity 63.6%; Pred. No. 1.3e-50;
 Matches 505; Conservative 0; Mismatches 274; Indels 15; Gaps 2;
 QY 309 ATCTTCATGAAGACCGGAGACAGAGATTGATGAGCGGCGAGAGTGAGCCGTC 368
 DB 96 ATGACATGAACTACCCCGCTGAACCGAATTCCAACAGGCTTACGAGAGCTTACAC 155
 QY 369 TCCTCTGCA-----GCCCGTTTGAAGAGCGCCCGAGCTGCTGCCCATTTCAACAG 422
 DB 156 TCCATTCACGACTGCTGTTGACAGACCCCGAGTTCGAAAGTTCATCCCTGTG 215
 QY 423 ATCTTGAAGCTGAGCGGATGATCACTTCGCGGTCCTGAGAGAGAGCGGAGAC 482
 DB 216 GTGCTGTTCTGAGCGAATCATCAAGTTCGAGTGTGTGGAGAGAGACAGAGGCAAG 275
 QY 483 CTGACAGTCAACCGCGCTTCCGCGTGAAGTACTGTCGCGCATCGGCCCTACAGGGC 542
 DB 276 CTGACAGTCAACCGTGGCTACGAGTCAAGTCAACTCGCTCGGCGCTTACAGGGA 335

QY 543 GACCTGGCTTCCACCCCTCGTGAACCTGTCATGAGTTCCTTGACCTTGGACAG 602
 DB 336 GGTTCGATTCACACCTTCCGTCACCTGTCATCTTCAAGTTCTCGATAGAGAC 395
 QY 603 ATCTTCAAGAACGCTTACACCTGTCATGAGCGCGGAGAGAGAGAGAGAGAGAG 662
 DB 396 ATCTTCAAGAACGCTTACACCTGTCATGAGCGCGGAGAGAGAGAGAGAGAGAG 455
 QY 663 GACCCCAAGGCAAG 722
 DB 456 GACCCCAAGGCAAG 515
 QY 723 CTGAGAGGCAATGAGTGTGCTGACATGATGTCCTGCGGAGAGAGAGAGAGAG 782
 DB 516 CTGACAGACACATGAGTGTGCTGACATGATGTCCTGCGGAGAGAGAGAGAGAG 575
 QY 783 CGCAGATTGCTTACCTTTTCGAGCAGTACAGAGAGAGAGAGAGAGAGAGAGAG 842
 DB 576 CGAGAGTGTGCTTCTTCTGCGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 635
 QY 843 CTGACCCCAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 902
 DB 636 CTGACCCGTAAGGCTGACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 695
 QY 903 GCGCGCTGCTGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
 DB 696 GGTCTCTTACTACGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 755
 QY 954 AAGGCAAG 1013
 DB 756 AAGGCAAG 815
 QY 1014 CTGCTGAG 1073
 DB 816 GTCAATGAGTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 875
 QY 1074 CCACAGCGCTTAC 1087
 DB 876 GTCTCGACTTAC 889

RESULT 7
 LOCUS BW480553 854 bp mRNA linear EST 11-JUN-2004
 DEFINITION BW480553 Nori Satoh unpublished cDNA library, mature adult whole
 animal Ciona intestinalis cDNA clone cima038a08 5', mRNA sequence.
 ACCESSION BW480553
 VERSION
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Plebobranchia; Clonidae; Ciona.
 REFERENCE 1 (bases 1 to 854)
 AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
 TITLE Expressed genes in Ciona intestinalis (2004)
 JOURNAL Unpublished (2004)
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-1113
 Email: satoh@acidian.zool.kyoto-u.ac.jp.
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 /clone="cima038a08"
 /issue_type="whole animal"
 /dev_stage="mature adult"

ORIGIN /clone_1lb="Nori Satoh unpublished cDNA library, mature adult whole animal"

Query Match 13.7%; Score 292.4; DB 5; Length 854;
 Best Local Similarity 60.2%; Pred. No. 5.7e-48;
 Matches 479; Conservative 0; Mismatches 317; Indels 0; Gaps 0;

QY 289 TGGCCAGCTGCTGACCGAGATCTTCATGAAAGACCCGGAGCAGCAGAGTTCATGACAG 348
 DB 22 TGGACCAAGTCAAGCTTAAAGTAAAGAGAGAGATCCAAACCAACTGAGTTTTCACAG 81
 QY 349 CGGTGCGCAGAGTGGCCCTCTCCCTGACGCCGCTTTCAGAGAGCCGCCAGCTGCTGC 408
 DB 82 CGGTGACAGAGTCTCATTTTCATTTGAACCGTTATTCGCTACCCCAAGTACTGT 141
 QY 409 CCATCTTCAGCAGATGTTGAGCTTGAGCCGCTGATCATTCCGCTGCTCTGCTGG 468
 DB 142 CAGTTTTCAGCAGATGTCAGGCCAGAAAGGTGTGACAAATTCGAGTACCATGCGAGG 201
 QY 469 ACGAGCCGCGCACTGAGGTCAACCGCGCTTCGCGGTGACAGTACCTCGCCGCAATCG 528
 DB 202 ATGACAAAGGTGACATACAAATTAACGAGGCTTCAGATCAGTTTAATCAGGCGCATTC 261
 QY 529 GCCCTTCAAGAGGGCGCTGCGCTTCAACCCCTCCGTAACCTGTCATCAATGAAGTTCC 588
 DB 262 GCCCGTCAAGAGGGCGCTGCGTTTCCACCCTCGTCAATCTGTCATCATCAAGTTTC 321
 QY 589 TTGCTTTGAGAGATCTTCAGAAACAGCCCTGACACCTTCCATGCGGCGGCGCAAG 648
 DB 322 TGGGCTTCAGAGCAATTTTAAAGACGACCTCAGACATTCCAATGGAGGCGGCAAG 381
 QY 649 GCGGCTCCGACTTCGACCCCAAGGAGCAGAGCGGAGGTGATGCGCTTTCGCCAGT 708
 DB 382 GTGGGTGCGATTTGATTCGAAAGGAAACAGACAGAGTCTCAGGTTTTCGACAG 441
 QY 709 CTTTCATGACCGAGCTCAGCGCCCAATCAGTACGTGACAGAGCTGCCCGCGGACCA 768
 DB 442 GCTTCATGACGAGATTTGTTCAACACATTTGCGCGATACGAGCTGCCGCTGGAATTA 501
 QY 769 TCGGCGTGGGCGCGCGAGATTGGCTACCTTTTCGCGCAGTACAAAGCATCACAGAA 828
 DB 502 TTGGGGTTCGGGGGTGAGAAATTTGGCTTCATGTTGACAGTACAAACGATTTTCAACT 561
 QY 829 ACTACACCGGCTGCTGACCCCAAGGAGCAGAGTATGCGGCTCCGAGATTCGCCCGC 888
 DB 562 GCCACCAAGAGTCTGACCGGTAAAGATGGGTTGGGAGGTTCCCTTATACAGACAG 621
 QY 889 AGGCAACCGCTACGCGCGCTGCTGTTTGTGAGAAAGTGTGAGAGACAAAGGCGAGA 948
 DB 622 AAGCAACAGGTTACGGAATGGTGTACGCGCTCGACTTTGCGATGAAGATGTCCGGGAAA 681
 QY 949 GCTTCAGAGGAGACCGCTGCTGTTCTGCGCGGCGCAAGTGGCCCAAGTACGCGCG 1008
 DB 682 GCTTCGCGGAGAAACGAGTACGTTATCTGGGTAAGTGGGCAAGTTCGCANCAN 741
 QY 1009 AGCTGCTGCTGAGAGAGCGCCATCGTCTGCTGCTGCCAGGAGGCTACAGTGT 1068
 DB 742 AANAATGTCTGAACTGTGTGCAACTGTCTTACTTCANCACTGTGCTGGAATCTTTT 801
 QY 1069 ACGAGCCCAACGCGCTT 1084
 DB 802 ACNANCCGAAAGGTTT 817

RESULT 8
 CV211068/c 943 bp mRNA linear EST 16-SEP-2004
 LOCUS EST870778 non-normalized T1 cDNA library Trichomonas vaginalis cDNA
 DEFINITION clone TVMBE13 3' end, mRNA sequence.
 ACCESSION CV211068
 VERSION CV211068.1 GI:52158048
 KEYWORDS EST.

SOURCE
 ORGANISM
 Trichomonas vaginalis
 Trichomonas vaginalis
 Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;
 Trichomonadidae; Trichomonadinae; Trichomonas.

REFERENCE
 AUTHORS
 Carlton, J.M., Dyall, S., Johnson, P.J. and Frazer, C.M.
 TITLE
 The complete genome sequence of the sexually transmitted parasite Trichomonas vaginalis
 JOURNAL
 Unpublished (2004)
 COMMENT
 Other ESTs: EST870779
 Contact: Jane Carlton
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208
 Email: carlton@igr.org
 Seq primer: polydT 24 base.
 Location/Qualifiers

FEATURES
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 /organism="Trichomonas vaginalis"
 /mol_type="mRNA"
 /strain="T1"
 /db_xref="taxon:5722"
 /clone="TVMBE13"
 /note="Vector: Lambda Triplex2; Site 1: SfiA; Site 2: SfiB; T. vaginalis strain T1 library constructed from cDNA, made in lambda Triplex2. Inserts cloned unidirectionally in the SfiA and SfiB sites. Mass excision of library produced inserts in pTriplex2 plasmid. Inserts sequenced from both 5' and 3' ends using Triplex2 sequencing primer and polydT 24 bp primer respectively."

ORIGIN

Query Match 13.5%; Score 288.6; DB 7; Length 943;
 Best Local Similarity 58.2%; Pred. No. 3.3e-47;
 Matches 548; Conservative 0; Mismatches 384; Indels 9; Gaps 2;

QY 690 GTGATGGCTTTCGCGACGCTTCATGACCGAGCTGAGGCGCACTCAGTACGTGCGAG 749
 DB 943 GTGATGAGATTCGCGACGATATTATGCTGGAATTCACGCCACATCGGCGCAACACA 884
 QY 750 GAGTGCCCGCGCGCGCATCGCGCTGCGCGCGAGATTGGCTACTTTTCGGCGAG 809
 DB 883 GATGTCCACAGAGTATATCGGTTGTGCTCGGAATTCGATACATGTTTCGGCGAG 824
 QY 810 TACAGGCGATCACCAAGAACTACACCGCGCTGACCCCGAAGGCGCAGAGTATGCG 869
 DB 823 TACAGGCGATCAAGAAAGTCTTCGAGGCGCTCTCAGGCAAGGCGCATCTCATTCGAT 764
 QY 870 GGCCTCGAGATTCGCGCGCGCGCGACCGGCTACGCGCGCGCTGCTGTTTGTGAGAAAGCTG 929
 DB 763 GGCCTACTGATTCGCTCAGAGATCACAGGCTACAGGCTTGTCTTACTTCATCAGAAATG 704
 QY 930 CTGAAGGACAAAGGCGAGACCTCAAGGGGCAAGCGCTGCTGATGTGCGCGCGCAAC 989
 DB 703 CTCGCTACTAAGGCGGAGAGATCAAGGGGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 644
 QY 990 GTGGCCAGTATGCGCGGAGCTGCTGCTGAGAAAGGCGCATCGTGTGCTGCTGCTGCTG 1049
 DB 643 GTGCAAGTATGCTGCTGCGAAGCTCATGCACTGCGCGCAATCCAGTCTCATGCTCA 584
 QY 1050 GACTCCAGGCGTACGTTACGAGCCCAAGGCTTACGCGCGGAGGAGCTGCGAGGGGTG 1109
 DB 583 GACTCACGCGCGCTCTCATCTTCAAGAGATGATGCAAGAGCATCTTATGCTGTC 524
 QY 1110 CAGGACATGAAGAAGAAACAACAGCGCGCGC-----ATCTCCAGTACAAAGAGCAG 1163
 DB 523 ATGCACATCAAGAAAGTGTGCTGCTGCAAGACTCAAGAAAGTTTCAAGAACTTCCAGAC 464
 QY 1164 ACCGCGGTATGTGGCGAGCCGCGCAAGCC--TTGGAGCTGAGCTGCGCAGGTGGAC 1220

Db	Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Comment	Features	Source
Db	463	CTCAAGGCGTACGAGTACATGATGGAAGTCATCATCTGGGCGCTGGGAAGTTCCATGCCAT	401								
Qy	1221	ATGCGCTTCCCTTGGCGCCACCCAGAAAGATGATGAGCAAGAGCGGAGCTGCTATC	1286								
Db	403	ATGGGTCTTCCATGTGCTACACAGAACGAAATTCCTCCAGAGCACTTTCATCATGTGTC	344								
Qy	1281	AAGCAGCGGTGCGATGATCGTGTGGAGGGCGCCAACTATGCCCTCCACCAAGAGGCCATC	1340								
Db	343	AAGAAACGGGCTCAGCTCTCGCAGAAAGTGTCTTAACATGCAATCAACAAACGACGAAATC	284								
Qy	1341	CACAAAGTCAACAAAGCGCGGCATCATCTACTGCCCCCGGACAGCGCGCAACCGCGCGAC	1400								
Db	283	GAGCTCTACATGAAGAGAAACATCTACTACGCGCCAGGAGGAGCAACGCCCGGTGT	224								
Qy	1401	GTGGCGGTACAGCGCGCTTGAGATGACCAGAACCGCATGAGCTGTAACCTGACTCGCGAG	1466								
Db	223	GTTCCTGTCTCAGGTCTCGAAATGACAGAAACAGCTGCTCGATGCTATCCGAC	164								
Qy	1461	GAGGTTCGCGAACACTGTGAGGCGCATCATGAAAGCATCTACGACTCCGCCATGGGGCGG	1522								
Db	163	AAGGTGCAAGAAACCTCAAGGAAATCATGCAACATCTTGGAAGCGCGCCATTCCTCC	104								
Qy	1521	TCCCCAGATACAACTGTGACCTGTGCTGGCGGCGGCAATCGCGGGCTTCAACAAAGTG	1580								
Db	103	AGTAGGACGATATGTGTTCTTCACTACAAAGGATGCGCAACCTTGCGGGCTTCAAGCTGTT	44								
Qy	1581	GCTGATGCCGTCAAGGCCAGGCGCGCTGTTAAGCTGCCCA	1621								
Db	43	GCCGATGCTATGTCTTGCCCTAGCGGCTGTGCTAAGCTAGCGA	3								
RESULT 9	AUI86881	540 bp	mRNA	linear	EST 14-OCT-2003						
LOCUS	AUI86881	Porphyra yezoensis TU-1 sporophytes	Porphyra yezoensis								
DEFINITION	AUI86881	CDNA clone PF005C01_r 5', mRNA sequence.									
ACCESSION	AUI86881										
VERSION	AUI86881.1	GI:31919960									
KEYWORDS	EST.										
SOURCE	Porphyra yezoensis										
ORGANISM	Porphyra yezoensis										
REFERENCE	1	(bases 1 to 540)									
AUTHORS	Asamizu,E., Nakajima,M., Kitade,Y., Saga,N., Nakamura,Y. and Tabata,S.										
TITLE	COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS										
JOURNAL	J. Phycol. 39 (5), 923-930 (2003)										
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yama 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.										
FEATURES	location Qualifiers										
source	1..540										
	/organism="Porphyra yezoensis"										
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	/clone="PF005C01_r"										
	/dev_stage="sporophytes"										
	/clone_1kb="Porphyra yezoensis TU-1 sporophytes"										
ORIGIN											
Query Match	13.2%	Score 282.8;	DB 1;	Length 540;							
Best Local Similarity	70.6%	Pred. No. 4.6e-46;									
Matches 377;	Conservative	0;	Mismatches 157;	Indels	0;	Gaps	0;				
468	GACGACGCGCGCAACCTGCAAGTCAACGCGCGCTTCGCGTGCAGTACTCTCGGCCATC	527									

QY 528 GGGCCCTTCAAGAGGGGGGGCTGGCTTCCACCCCTCGGAACCTGTGCATCATGAAAGTTC 587

Db 65 GGGCCGTCAMAGGGGGGGCTTGTCTTCAACCTTACCGTGAACCTTCTCATCTCCAAAGTTC 124

QY 588 CTTCGCTTTGAGCAGATCTTCAAGAAACGCTGACCACTCGGCCATGGGCGGGCGAAG 647

Db 125 CTTCGGAACGAGACAGGTGCTGTGAAGAACCCGCGTAGACCTCTCGCTTGGGCGGGCAAG 184

QY 648 GGGCGCTCCGACTTCGACCCCAAGGGGCAAGACGACGGGGAGGTATGGCGTTCTTGGCAG 707

Db 185 GGGGGGTCTGATTTTAACCTTAAGGGGGCGCTCCGAGGGGAAGTGTGTGCTTTTGGCCAG 244

QY 708 TCCTTCATGACCGAGACTGACAGCGGCACATCAAGCTACGTGCAGAGAGTGGCCGCGCGAGC 767

Db 245 TCCTTCATGAGGTGCCCTGGCTCGCACATTTGGTCCGACACAGGAATGTTCCGGCGGGTGAC 304

QY 768 ATCGCGCTGGGGCGCGCGCGAGATTGGCTACTTTTCGGCAGTACAAGCGCATCACCAAG 827

Db 305 ATTGGGGTGTCCGGAACGGGAAGATTGGCTACTCTGTTTGGCGGCTACAAAGGCGCTGACCAAC 364

QY 828 AACTACACCGGGGTGTGACCCCGGAAGGGACGAGATATGGCGGGCTCCGAGATTCGGCCCC 887

Db 365 CGCTTTGAGGGCATCTCTACCGGGCAAGGGTCTTACGTTTGGGGGCGTCCCTCATTTGGCCTT 424

QY 888 GAGGCGACCGGCTACGGGGCGCGGTGCTGTTTGTGAGAAAGTGTCAAGAGACAAAGGCGGAG 947

Db 425 GAGTGCACAGGGTATGGCGTGTGATCATGTTTGTTCGTGAGATGCTCAAGGTCAAGGGCGCAT 484

QY 948 AGCCTCAAGGCAAGCGCTGCTGTGTGTCTGGCGGGGCAACGTGGCCCAAGTAC 1001

Db 485 ACGCTGAAGGCAAGGTGTGTGTATCTCCGGCAAGTGGCAACGTGCCCCAAGTAC 538

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RESULT 10
LOCUS      CL693787
DEFINITION CL693787      820 bp      DNA      linear      GSS 10-JUL-2000
ACCESSION  PR10162C.B08.2 - PR10162C.BR (820) Mixed stadge fosmid library of P
VERSION     pacificus var. Californa Pristionchus pacificus genomic, genomic
KEYWORDS    survey sequence.
SOURCE      CL693787
ORGANISM    CL693787.1 GI:50215695
            GSS.
            Pristionchus pacificus
            Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1 (bases 1 to 820)
AUTHORS     Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE       AppadB: an Acedb database for the nematode satellite organism
            Pristionchus pacificus
COMMENT     Nucleic Acids Res. 32 (1), D421-D422 (2004)
            Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@uebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             location/Qualifiers
     source            1..820
                        /organism="Pristionchus pacificus"
                        /mol_type="genomic DNA"
                        /strain="Californa"
                        /db_xref="taxon:54126"
                        /clone_lib="Mixed stadge fosmid library of P. pacificus
                        var. Californa"
                        /note="Vector: pBplfos-5 Fosmid vector"
ORIGIN

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Query Match 13.1%; Score 281; DB 9; Length 820;
 Best Local Similarity 62.5%; Pred. No. 1.1e-45;
 Matches 437; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 402 CTGCTGCCCATCTTCAAGCAGATCGTTGAGCGCTGATCACTTCGGGTGCC 461
 DB 91 CAGATGTCATTAATGAGCGTCTGTGTAACCGAGCGCGTATCGAGTTTCGGGTGA 150
 QY 462 TGGCTGACGACGCGGCAACCTGACAGTCAACCGCGCTTCGCGTGCAGTACTCGTCC 521
 DB 151 TGGGTGATGATCGCAACAGATACAGTCAACCGTGTATGCGTGTGCACTTCAAGCTT 210
 QY 522 GCCATCGGCGCCCTCAAGAGCGGCGCTGCTTCCACCCCTCCGTGAACCTGTCATCATG 581
 DB 211 GCCATCGGCGCCCTCAAGAGCGGCGTATGCGCTTCCATCCGTATTAACCTTTCATCTC 270
 QY 582 AAGTTCCTTGCCTTGAAGCAGATCTTCAAGAACGCTGACCACTTCCCTCCATGAGCGGC 641
 DB 271 AATTTCTCGGCTTTGAACCAACCTTCAAAAATGCCGTGATCCCTGCTGCGCGATGGCGGT 330
 QY 642 GCGAAGGCGGCTCGACTTGAACCCCAAGGCGAAGCGCAGAGGTGATGCGCTTC 701
 DB 331 GGTAAAGCGGCGACGATTTGATCCGAAAGAAAAGCGAAGGTGAAGTATCGCTTTT 390
 QY 702 TGCCAGTCTTCAATGACCGAGCTGACGCGCCACATCACTACGTGACAGAGCGTCCGCC 761
 DB 391 TGCCAGGCGCTGATGACCGAGCTTTATGCTATCTGCGCGCGGATCCGAGCTTCCGCCA 450
 QY 762 GCGCAATCGGCGTGGCGCGCGAGATGAGTGGCTACTTTTCCGCCAGTACAGCGCATC 821
 DB 451 GGTATATCGGGGTGGTGGTGTGTAAGTCCGCTTTATGCGGGGATGATGAAAAAGCTC 510
 QY 822 ACCAAGAACTACACCGCGTGTGACACCCGAAAGGCGCAGATATGAGGCGTCCGAGATC 881
 DB 511 TCCAACATACCGCGCTGCTTCAACCGTAAGGCGCTTCAATTTGGGCGCATTTATT 570
 QY 882 CGCCCCGAGCGACCGGCTACCGCGCCGCTGTTTGGAGAAAGTGTGAAGAAAG 941
 DB 571 CGCCCCGAGCGTACCGGCTACCGGTCTGTTTATTTCAAGAAAGATTTAAAGCGCAC 630
 QY 942 GCGCAGAGCTCAAGAGCGCAGCGCTGCTGTGTGTGGCGGCGCAAGTGGCCAGTAC 1001
 DB 631 GGTATGGGTTTGAAGGATCGCGTTCGCTTTCGGCTCCGCAAGTGGCCAGTAC 690
 QY 1002 TGCCGCGAGCTGCTGTGAGAGAGGCGCCATCGCTGTGCTGCTCCGATCCCAAGGC 1061
 DB 691 GCTATCGAAAAAGCGATGAAATTTGTGCTGCTGTGATCACTGCGTCAAGCTCCAGCGC 750
 QY 1062 TACGTGTACGAGCCCAACGCGCTTACGCGCGAGCAGCTG 1100
 DB 751 ACTGTAGTTGATGAAGCGGATTCACGAAGAAAGAACTG 789

RESULT 11
 CF839891 638 bp mRNA linear EST 30-OCT-2003
 LOCUS pshB004xpf07f USDA-IRAFS:Expression of Phytophthora sojae genes
 DEFINITION during infection and propagation_sshB Phytophthora sojae cDNA clone
 SHB004F07 5, mRNA sequence.

ACCESSION CF839891
 VERSION CF839891.1 GI:38055545
 KEYWORDS EST.

SOURCE Phytophthora sojae
 ORGANISM Phytophthora sojae
 Eukaryota; Stramenopiles; Oomycetes; Pythiales; Pythiaceae;

REFERENCE 1 (bases 1 to 638)
 AUTHORS Tyler B.
 TITLE Unpublished (2003)
 JOURNAL Contact: Tyler B

COMMENT Tyler lab

VBI
 1880 Pratt Dr., Blackeburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmtyle@vt.edu

PCR Primers
 FORWARD: BK reverse primer
 BACKWARD: BK reverse primer
 Plate: 004 row: F column: 07
 Seq primer: BK reverse primer
 High quality sequence stop: 638.

FEATURES

source

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 /cell_line="P6497"
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 /lab_host="Soybean plant"
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 genes during infection and propagation_sshB"
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ORIGIN

Query Match 12.8%; Score 274.6; DB 7; Length 638;
 Best Local Similarity 66.7%; Pred. No. 2e-44;
 Matches 426; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 380 CGTGTTCGAGAGCGCCCGAGCTGCTGCCATCTTCAAGCAGATGTTGAGCTGAGCG 439
 DB 9 CGTGTTCGAGAGCGCCCGAGCTGCTGCCATCTTCAAGCAGATGTTGAGCTGAGCG 68
 QY 440 CGGATACCTTCGGGTGTCTGCTGAGAGAGCGCGCACTGAGGTCAACCGCG 499
 DB 69 CGGATACCTTCGGGTGTCTGCTGAGAGAGCGCGCACTGAGGTCAACCGCG 128
 QY 500 CTTCCGCGTCACTGCTGCTGCGCCATCGGCGCCCTCAAGAGGCGGCTGCGCTTCCACC 559
 DB 129 CTTCCGCGTCACTGCTGCTGCGCGCGCTGCGCGCTGCGCTGCGCTTCCACC 188
 QY 560 CTCCTGTAACCTGTCACTATGAAGTTCTTGCCTTTGAGCAGATCTTCAAGAAAGCCT 619
 DB 189 GGAAGCAACCGAGCGCATCCCAAGTTCTGCGCTTCAAGCAGATCTTCCGCAACGCGCT 248
 QY 620 GACCACTTCCATGAGCGCGCGCGCAAGCGGCGCTCGACTTGAACCCCAAGGCAAGAG 679
 DB 249 GCGCGGCGCTGAC--GCGCGCGCGCGCGCGCTGCGACTTGAACCCCAAGGCAAGAG 305
 QY 680 CGAGCGAGAGTATGCGCTTTCGCGAGTCTTCAATGACCGAGCTGCGAGCGCCATCAG 739
 DB 306 CGAGTGGAGATCATGCGCTTTCGCGAGTCTTCAATGACCGAGCTGCGAGCGCCATCAG 365
 QY 740 CTAAGTACAGAGCGTCCGCGCGCGCGCATGCGCGTGGCGCGCGAGATTGGCTACT 799
 DB 366 CCGCACAACAGAGTGGCCCAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 425
 QY 800 TTTCCGCGATTAAGAGCGATCAACCAAGATCAACCGCGGTCTAGACCCCGAAGGCGCA 859
 DB 426 GTTCCGCAATTAAGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
 QY 860 GAGATATGCGGCTCCGAGATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 919
 DB 480 TCTGATGAGAGCGGCTTACACATCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 539
 QY 920 GGAAGAGTCTGAAGCAAGGCGAGAGCTTCAAGGCGAGCGCGCTGCTGTGTGG 979
 DB 540 CAACCGCATCTGGAAGAGCGCGAGAGAGCGTCAAGGCGAAGCGCTGCTGATTCGCG 599
 QY 980 CGCGGCGAAGTGGCCAGTACGCGGAGCTGCT 1018
 DB 600 CAGTGGCACCGTGGCGCTCAACGTGGCGCGCGAGAGCTGCT 638

RESULT 12
LOCUS BM436105 727 bp mRNA linear EST 03-JUN-2004
DEFINITION BM436105 Nori Satoh unpublished cDNA library, juvenile whole animal
Ciona intestinalis cDNA clone cijv03107 5', mRNA sequence.
ACCESSION BM436105
VERSION BM436105.1 GI:48134395
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 727)
Satonou, Y., Nakayama, A., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2004b)
JOURNAL Unpublished (2004)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..727
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ORIGIN
Query Match 12.7%; Score 271.6; DB 5; Length 727;
Best Local Similarity 61.2%; Pred. No. 8.1e-44;
Matches 436; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

289 TGCAGCACTGCTGACCGAGATCTTCATGAAGAGCCGAGAGAGAGATTCATGACG 348
12 TGGAGCAAGTCAAGCTAAAGTACAGAGAGAGATCCAAACCAATGATTTTGACAG 71
349 CGGTGCGGAGGTGCGCTCTCCCTGACAGCCGCTTTCAGAGAGCGCCCGAGCTGCTGC 408
72 CGGTGAGAGAGGTGCTCATTTGATGAACCGTTATTCGATCGCTACCCCAAGTACTGT 131
409 CCATCTTCAAGCAAGTCTGAGCGCTGAGCGGTGATCACCTTCGCGCTGCTGCTGCG 468
132 CAGTTTTCAGAGCTGTCAGAGCGAGAGAGAGGTGTAACAATTCGAGTACCATGCGAG 191
469 ACGAGCGCGGCAACCTGAGGTGCAACCGCGCTTCGCGTGCAGTACTGTCGCCGATCG 528
192 ATGACAGAGGTGACATACAAATTAACCGCGCTTCAGAGTTCAGTTATCAGGCGCATG 251
529 GCCCTTACAGAGCGCGCTGCGCTTCACACCCCTCCGTAACTGTTCATGAAGTTCC 588
252 GCCCGTACAGAGCGGTGCGTTTCACACCATCGTCAATCTGTCAATCAATAAGTTTC 311
589 TTGCGTTGAGCAGATCTTCAAGAACAGCTGACACACCTGCGCAATGGCGCGCGCAAG 648
312 TGGGCTTGAGCAAAATTTTAAGAACGACATCACTTCCAATGGAGGCGCAAG 371
649 GCGGCTCCGACTTCGACCCCAAGGCGCAAGAGCGAGCGAGTGTGCTTTCGCCAGT 708
372 GTGGGTGATTTTGATCCAAAGGGAATACTGACAGGAGAGTTTTCAGTTTGCCAGA 431
709 CCTTATACAGGAGTGCAGGCGCACATCACTAGTACGTGACAGAGCTGCGCGCGGCA 768
432 GCTTCATACAGGAGTGTTCAAACACATTTGGCGCGGATACGAGCGTCCCGCTGGAGTA 491
769 TCGGCTGCGGCGCGCGAGATGTGCTACCTTTTCGCGCATGACAGGCGCATCACCAAG 828

DB 492 TTGGGCTGCGGCGGTGCAAAATTTGCTTCATGTTTGACAGTACAAAGTATTCAAACT 551
QY 829 ACTACACCGCGCTGCTGACCCCGAAGGCGCAGAGTATGCGGCTCCGAGATCCGCCCG 888
DB 552 GCCACCAAGAGGTGCTGACCGGTAAAGATGCGGTGGGAGTTCGCTTATACGACCAN 611
QY 889 AGGCAACCGCTAGCGGCGCGTGTGTTTGAGGAACGTGCTGAGGACAGGCGCGAGA 948
DB 612 AAGCAACAGTGTACGGGTGTGTTGACCGGCTCGACTTTCGATTAAGATGTCGAAANA 671
QY 949 GCTTCAAGGCGAAGCGCTGCGCTGCTGCTGCGCGCGGCAAGTGCACCATGAC 1001
DB 672 GCTTCCGCGGGAAGAAAGTACGATATCTGCTTCTGGGAACGTGCGACANTTC 724

RESULT 13
LOCUS BM438709 694 bp mRNA linear EST 03-JUN-2004
DEFINITION BM438709 Nori Satoh unpublished cDNA library, juvenile whole animal
Ciona intestinalis cDNA clone cijv403b07 5', mRNA sequence.
ACCESSION BM438709
VERSION BM438709.1 GI:48137422
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 694)
Satonou, Y., Nakayama, A., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2004b)
JOURNAL Unpublished (2004)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
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1..694
Location/Qualifiers
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ORIGIN
Query Match 12.6%; Score 270; DB 5; Length 694;
Best Local Similarity 62.0%; Pred. No. 1.7e-43;
Matches 423; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

318 AAGACCCGAGAGCGAGAGTTCATGACGCGGTGCGGAGTGGCCGCTCCCTGACG 377
12 AGGATCCAAACCAACTGAGTTCATGACGCGGTGACGAGGTCCTCATTTCAATGAAA 71
378 CCGGTGTTGAGAAAGCGCGAGCTGCTGCCATCTTCAAGCAGATCGTTAGACTGAG 437
72 CCGTATTTGATGCTCTACCCCACTACTTGTGCTAGTTTTCGACAGAGTGTGAGACCGA 131
438 GCGGTGATCACTTTCGCGGTGCTGCTGAGACGACGCGGCAACTGACAGTCAACCGC 497
132 AGGTTGTAATAATTCGAGTACATGACAGATGACAAAGGTGATCAATAATTAACGA 191
498 GGTTCGCGGTGATCTGCTCGCATGAGCGCCCTTACAAAGGCGGCTGCGCTTCCAC 557
192 GCTTCAGAGTCCAGTTTAATCAGGCGCATTTGGCGCGTACAAAGGAGGCTTGCCTTCC 251
558 CCGTCCGGAACCGTGCATCATGAATGCTTCTTTCGAGCAGATCTTCAAGAACGAG 617

Db 252 CTTTCGGTTAATCTGTCCATCATCAAGTTTCTGGGCTTCGAGCAAAATATTAAAGACCA 311
Qy 618 CTGACCACTCCCTGATGGGCGGCGCAAGGCGGCTCCGACTTCGACCCCAAGGCGAAG 677
Db 312 CTCACGACACTTCCATATGGAGGCGGCAAGGTGGTGCATTTTGATCCAAAGGAAAA 371
Qy 678 AGCGACCGGAGTGATGCGCTTCGCCAGTCTTCATGACCGAGCTGCACGCGCACATC 737
Db 372 ACTGACAGCGAAGTTCTCAGGTTTTCGAGAGCTTCATGACGAGTTGTTCAACACATT 431
Qy 738 AGCTACGTCAGAGAGTGTCCCGCGGCGACATCGGCGTGGCGCGCGGAGATTGGCTAC 797
Db 432 GGCCTGGATACCGAGCTCCGCTGAGATATTGGGGTGGGGGTGCAAGAAATGGCTTC 491
Qy 798 CTTTTCGCGCAGTCAAGCGCATCAACAAAGTACACCGGCGTGTGACCCCGAGGCGC 857
Db 492 ATGTTTGACAGTACAAAGTATTACAACTGCCACCAAGAGTGTCTGACCGGTAAAGGA 551
Qy 858 CAGAGTATGCGCGCTCCGAGATCCGCGCGGCGACCGGCTACGCGCGCTGCTGTTT 917
Db 552 TGGGGTTGGGAGGTTGGCTTATACNACNAAAGCAAGGTTAGGATGGTGAAGCG 611
Qy 918 GTGAGAACTGTCGAGAGCAAGGCGAGCCTCAAGGCGCAAGCCTGCTGTGCT 977
Db 612 CTCACCTTTGGGATGAAAGATGTCNGGGAAAGCCTTGGCGGAAAAACGCTGACGTATCT 671
Qy 978 GCGCGGCGCAAGTGGCGCCAGT 999
Db 672 GCTTCTGGGAAAGTGGCACANT 693

RESULT 14
LOCUS BM475527 730 bp mRNA linear EST 11-JUN-2004
DEFINITION BM475527 Nori Satoh unpublished cDNA library, mature adult whole animal Clona intestinalis cDNA clone clma014f19 5', mRNA sequence.
ACCESSION BM475527
VERSION BM475527.1 GI:48611391
KEYWORDS EST.
SOURCE Clona intestinalis
ORGANISM Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cloniidae; Clona.
REFERENCE 1 (bases 1 to 730)
AUTHORS Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
TITLE Expressed genes in Clona intestinalis (2004)
JOURNAL Unpublished (2004)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
source location/Qualifiers
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/clone="clma014f19"
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/dev_stage="mature adult"
/clone_lib="Nori Satoh unpublished cDNA library, mature adult whole animal"

ORIGIN
Query Match 12.6%; Score 269; DB 5; Length 730;
Best Local Similarity 61.2%; Pred. No. 2.7e-43;
Matches 434; Conservative 0; Mismatches 275; Indels 0; Gaps 0;
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Qy 349 CGGTGCGGAGGTGCGCGTCTCCCTGACGCGCGGTGTGAGAAAGCGCCCGAGCTGTGC 408
Db 82 CGGTGACGAGGTGCTCATTTTCATGTGAACCGTATTATTCGATTCGCTACCCCAAGTACTGT 141
Qy 409 CCACTTTCAAGCAGATGTTGAGCTGAGCGGCTGATCACTTTCGCGTGTCTGTGCTGG 468
Db 142 CAGTTTTCGAGAGTGTGCGAGCCAGAAAGGGTGTGATCAATTCGAGTACCATGTGCGAGG 201
Qy 469 ACAGACCGCGCAACCTGCAAGTCAACCGGCGCTTCGCGCGTGTGAGTACTGTCGCGCATCG 528
Db 202 ATGACAAAGGTGACATCAATTAACCGAGCTTCGAGTCCAGTTTAATCAGGCCATTG 261
Qy 529 GCCCTTCAAGGCGGCGCTGCGCTCCACCCCTCCGTAACCTGTCCATCATGAAAGTTTC 588
Db 262 GCCGTGCAAGGAGGCTTTCGTTTCATTCATTCATTCGATTCGATTCATCATCAAGTTTC 321
Qy 589 TTGCTTTGAGCAGATTTTCAAGAACGCTGACACCTGCGCCATGAGGCGGCGCAAG 648
Db 322 TGGGCTTCGAGCAAAATATTAAAGACGCACTACACACTTCCAAATGGAGGCGGCGCAAG 381
Qy 649 GCGGCTCCGACTTCGACCCCAAGGCGAAGCGACGCGGAGTGTGCGCTTCCGCGAGT 708
Db 382 GTGGGTGCGATTTTGTGATCCAAAGGAAAACTGACAGCGAAATTTCTAGGTTTGGCAGA 441
Qy 709 CTTTATGACCGAGCTGACGCGCACATCACTACGTACGTCAGACGTCGCCGCGCGCAGA 768
Db 442 GCTTCATGACGAGTGTGTTCAAAACACTTGGCCCGGATACCGAGTCCCGCTGAGAGATA 501
Qy 769 TCGGCTGCGCGCGCGCGAGATTGGCTACTCTTTTCGCGCAGTACAAAGCATCAACAGA 828
Db 502 TTGGGGTTCGGGGGTCGAGAAATGGCTTTCATGTTTGGACGTCACAAAGTATTACAACT 561
Qy 829 ACTACACCGCGTGTGACCCCGAAGGCGCAGAGTATGCGGCTCCGAGATCCGCGCG 888
Db 562 GCACCAAGGAGTGTGACCGGTAAAGATGGGGTGGGAGGTTGCTTATACGACAG 621
Qy 889 AGGCAACCGGCTACGCGCGCGCTGTTTGTGAGAACGTGTGAAGAACAAAGGCGCAGA 948
Db 622 AAGCAAGGTTACGATTTGTGTAGCGGCTGCACTTTGGAGTAAAGATGTGGGGAAA 681
Qy 949 GCCTCAAGGCGAAGCGCTGCTGTGTGTGCGCGCGCAACGTGGCCCA 997
Db 682 GCCTTGGCGGAAAAACGTCGATCTGTGTTCTGGGAACGTGGCACA 730

RESULT 15
LOCUS AUI96696 527 bp mRNA linear EST 15-OCT-2003
DEFINITION AUI96696 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis cDNA clone PFL093d06_r 5', mRNA sequence.
ACCESSION AUI96696
VERSION AUI96696.1 GI:31939591
KEYWORDS EST.
SOURCE Porphyra yezoensis
ORGANISM Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
REFERENCE 1 (bases 1 to 527)
AUTHORS Aasamizu, S., Nakajima, M., Kikade, Y., Saga, N., Nakamura, Y. and Tabata, S.
TITLE COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG FREQUENCY ANALYSIS
JOURNAL U. Phycol. 39 (5), 923-930 (2003)
COMMENT Contact: Erika Aasamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1537-3, Kisarazu, Chiba 292-0812, Japan
Email: aasamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
source location/Qualifiers
1..527
/organism="Porphyra yezoensis"

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/db_xref="taxon:2788"  
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/dev_stage="sporophytes"  
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ORIGIN

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Query Match      12.4%; Score 266; DB 1; Length 527;  
Best Local Similarity 69.3%; Pred.No.1.1e-42;  
Matches 362; Conservative 0; Mismatches 160; Indels 0; Gaps 0;  
  
QY 380 CGTGTTCGAGAGCGCCCGAGCTGCTCCCATCTTCAAGCAGATCGTTGAGCTGAGCG 439  
DB 6 CGAGGCTGAGGGCGCGCAGAGTTTATTCAGTCAACAGCGCTGTTGAACCGGAGCG 65  
  
QY 440 CGTGATCACTTCCGCGTGTCTGCTGAGCAGACCGCGGCAACTGAGGTCAACCGCGG 499  
DB 66 TGTCAATCCAGTTCCGGGTGCTGCTGATGACGATGACCGGGGAGCTGCAAGTCAACCGCGG 125  
  
QY 500 CTTCCGCGCTGAGTACTGCTGCTCCCATGCGCCCTACAAAGGCGGCTGCGCTTCAACC 559  
DB 126 CTTCCGCGCTGAGTAACTCTGCGATGGGCGGTAAGGCGGCTTCTTCAACC 185  
  
QY 560 CTCCGTGAACCTGTTCATCATGAGTCTTCTTGAAGCATCTTCAAGACAGCCT 619  
DB 186 TACGTGAACCTCTTCATCTTCAGATTCCTTGCGAGCAGAGTGTGAAGAACGCGCT 245  
  
QY 620 GACCACTCTGCGCCATGAGCGCGCGGCAAGGCGGCTCCGACTTCGACCCCAAGGCGAGAG 679  
DB 246 GACGACTCTGCGCGTGGCGGCGGCGGCAAGGCGGCTGATTTCAACCTTAAGGCGCGCTC 305  
  
QY 680 CGAGCGGAGGATGATGCGCTTCTGCACTCTTCAAGCAGAGCTGACGCGCACATCAG 739  
DB 306 CGAGCGGAGGATGCGCTTCTTTCAGTCTTCAAGTGGTGGCTGCGCTGCGCACATTCG 365  
  
QY 740 CTACGTGAGGAGCGTGGCGCGCGGAGCATGCGGCTGAGCGCGGCGAGATTGGTACTT 799  
DB 366 TCCCGACACGAGATGTTCCGGCGGAGTGAATGGGATTCGCGGACGAGATTTGGTACTT 425  
  
QY 800 TTTGCGGCAGTACAGCGCATCACCAAGACTACACCGGCGTGTGACCCCGAAGGCGCA 859  
DB 426 GTTTGGCGGCTACAGCGCGTGAACCAACCGCTTTGAGGGCATCTCACGCGGCAAGGCTCC 485  
  
QY 860 GGAATATGCGCGCTTCCGAGATCCGCGCCGAGGCGCACCGGCTA 901  
DB 486 TACGTTTGGGGGCTCCCTCATTCGCTGAGTCAAGGAGTCA 527
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Job time : 6266 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 18:21:52 ; Search time 164 Seconds
(without alignments)
1240.463 Million cell updates/sec

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2720
Perfect score: 1 MGTALVAKPIVAAPLAAAPR.....GANTAGFTKVAIVAKQAV 526
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq.16Dec04:.*
1: Genesegp1980s:.*
2: Genesegp1990s:.*
3: Genesegp2000s:.*
4: Genesegp2001s:.*
5: Genesegp2002s:.*
6: Genesegp2003as:.*
7: Genesegp2003bs:.*
8: Genesegp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2720	100.0	526	2	AAW15407 NADP-spec
2	2720	100.0	526	5	AAU98950 NADP-gluc
3	2720	100.0	526	8	ADQ36707 NADP-spec
4	2621	96.4	512	2	AAW15408 NADP-spec
5	2621	96.4	512	5	AAU98951 NADP-gluc
6	2621	96.4	512	8	ADQ36709 NADP-spec
7	2508	92.2	487	5	AAU98954 Mature NA
8	2508	92.2	487	8	ADQ36729 Mature NA
9	2500	91.9	487	2	AAW15411 NADP-spec
10	2465	90.6	476	2	AAW15412 NADP-spec
11	2465	90.6	476	5	AAU98955 Mature NA
12	2465	90.6	476	8	ADQ36731 Mature NA
13	1309	48.1	445	6	ABU38763 Protein e
14	1309	48.1	450	7	ABO71900 Pseudomon
15	1300.5	47.8	444	8	ADP08330 Neisseria
16	1297.5	47.7	444	6	ABP77942 N. gonorr
17	1297.5	47.6	444	6	ABU37205 Protease
18	1294.5	47.6	444	6	AAU72986 Neisseria
19	1294.5	47.6	444	6	ABU38117 Protein e
20	1287.5	47.3	449	6	ABU39614 Protein e
21	1281	47.1	445	8	ADN24914 Bacterial
22	1259	46.3	454	8	ADN27186 Bacterial
23	1257.5	46.2	462	6	ABU17276 Protein e
24	1257.5	46.2	467	6	ADN34438 Acinetoba
25	1250.5	46.0	448	5	ABP65630 Bifidoba

26	1239.5	45.6	448	6	ABU29386	Abu29386 Protein e
27	1239.5	45.6	448	8	ADH97147	Adh97147 E. faecal
28	1239	45.6	449	5	AAU91467	AAU91467 Haemophil
29	1238	45.5	449	4	AAH88536	AAH88536 Haemophil
30	1238	45.5	449	6	ABU30172	ABU30172 Protein e
31	1236.5	45.5	449	5	ABP28423	ABP28423 Streptoco
32	1234.5	45.2	448	7	ADH85999	Adh85999 Enterococ
33	1230.5	45.2	449	6	ABU44405	ABU44405 Protein e
34	1230	45.2	449	6	ABU38946	ABU38946 Protein e
35	1221	44.9	448	8	ADK47974	ADK47974 Streptoco
36	1214	44.6	448	6	ABU46100	ABU46100 Protein e
37	1212	44.6	448	6	ABU01740	ABU01740 S. pneumo
38	1211.5	44.5	448	8	ADH97149	Adh97149 E. faecal
39	1210.5	44.5	458	8	ADS28251	ADS28251 Bacterial
40	1207.5	44.4	464	6	ABU23354	ABU23354 Protein e
41	1205.5	44.3	424	8	ADN17964	ADN17964 Bacterial
42	1205.5	44.3	444	6	ABU20518	ABU20518 Protein e
43	1204	44.3	447	2	AAW08092	AAW08092 Glutamina
44	1201	44.2	447	2	AAW60830	AAW60830 E. coli g
45	1201	44.2	447	6	ABU15360	ABU15360 Protein e

ALIGNMENTS

RESULT 1
AAW15407 standard; protein; 526 AA.
ID AAW15407;
AC AAW15407;
XX
XX
DT 17-OCT-2003 (revised)
DT 10-JUL-1997 (first entry)
XX
XX
DE NADP-specific glutamate dehydrogenase alpha-subunit precursor.
XX
XX
KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
KW chloroplast; transgenic plant.
OS Chlorella sorokiniana; strain UTEX 1230.
XX
XX
PN MO9712983-A1.
XX
XX
PD 10-APR-1997.
XX
XX
PF 03-OCT-1996; 96WO-US015921.
XX
XX
PR 06-OCT-1995; 95US-00541033.
XX
XX
PA (UYFL) UNIV FLORIDA.
XX
XX
PI Schmidt RR, Miller P;
XX
XX
PS WPI: 1997-226226/20.
XX
XX
DR N-PSDB; AAT64529, AAT64542.
XX
XX
PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
PT plant cells.
XX
XX
PS Claim 1, Page 25-27, 61pp; English.
XX
XX
CC 2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha
CC (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-
CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase
CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha
CC and beta subunits (see also AAW15411-12) that comprise the active NADP-
CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated
CC (pref. increasing the assimilation of inorganic N into organic N) by
CC transforming them with nucleotide sequences (see also AAT64529-30,
CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
CC proteins. Such plants show improved properties, e.g. increased crop yield
CC and improved stress tolerance. Heterohexamers having alpha and beta

CC subunits can be expressed that have higher aminating/deaminating activity
CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 526 AA;

Query Match 100.0%; Score 2720; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-250;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVAAPLAPRCLAPWPCAMVRSARVDRAKAVSLBEQISAMDATTTGDTFA 60
DB 1 MOTALVAKPIVAAPLAPRCLAPWPCAMVRSARVDRAKAVSLBEQISAMDATTTGDTFA 60
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DB 61 LOKAVKOMATKATGEGVLHGINKPVDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120
QY 121 RPELLPIFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRFPHSVNL 180
DB 121 RPELLPIFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRFPHSVNL 180
QY 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVMRCQSFMTLQRIHSYVD 240
DB 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVMRCQSFMTLQRIHSYVD 240
QY 241 VPAGDIGVAREIGLFGQYKRITKNYTGVLTPKQGEYGSSEIRPEATGGAVALFVENVL 300
DB 241 VPAGDIGVAREIGLFGQYKRITKNYTGVLTPKQGEYGSSEIRPEATGGAVALFVENVL 300
QY 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360
DB 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360
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DB 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPATQNEIDEHDAELLIKHGC 420
QY 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTQNRMSLNTWTRREVRD 480
DB 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTQNRMSLNTWTRREVRD 480
QY 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANITAGFTKVADAVAKGAV 526
DB 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANITAGFTKVADAVAKGAV 526

RESULT 2
AAU98950 standard; protein; 526 AA.

AC AAU98950;
DT 24-SEP-2002 (first entry)
DE NADP-glutamate dehydrogenase alpha subunit.
XX NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
XX ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
OS Chlorella sorokiniana.
FN US2002062495-A1.
XX 23-MAY-2002.
PD 23-MAY-1998; 98US-00070844.
XX 01-MAY-1998; 98US-00070844.
FR 01-MAY-1998; 98US-00070844.
XX (SCHMIDT R R.
PA (MILLER P.
XX (MILLER P.

XX Schmidt R, Miller P;
PI WPI; 2002-499691/53.
XX DR N-PSDB; ABK51007.
XX DR

PT Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
PT tolerance.

XX Claim 6; Page 13-15; 35pp; English.

CC The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transforming a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants with increased yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the amino acid sequence of Chlorella
CC sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the
CC method of the invention

XX Sequence 526 AA;

Query Match 100.0%; Score 2720; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.3e-250;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVAAPLAPRCLAPWPCAMVRSARVDRAKAVSLBEQISAMDATTTGDTFA 60
DB 1 MOTALVAKPIVAAPLAPRCLAPWPCAMVRSARVDRAKAVSLBEQISAMDATTTGDTFA 60
QY 61 LOKAVKOMATKATGEGVLHGINKPVDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120
DB 61 LOKAVKOMATKATGEGVLHGINKPVDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120
QY 121 RPELLPIFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRFPHSVNL 180
DB 121 RPELLPIFKQIVPEPRVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRFPHSVNL 180
QY 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVMRCQSFMTLQRIHSYVD 240
DB 181 SIMKFLAFEQIFKNSLITLPMGGGKGSDFDPKGSDAEVMRCQSFMTLQRIHSYVD 240
QY 241 VPAGDIGVAREIGLFGQYKRITKNYTGVLTPKQGEYGSSEIRPEATGGAVALFVENVL 300
DB 241 VPAGDIGVAREIGLFGQYKRITKNYTGVLTPKQGEYGSSEIRPEATGGAVALFVENVL 300
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DB 301 KDKGESLKGKRCIVSGAGNVAQYCAELLEKGAIIVLSLSDQGYVEBNGFTREQLQAVQ 360
QY 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPATQNEIDEHDAELLIKHGC 420
DB 361 DMKKKNSARISEYKSDTAVYVGDRRKPEWELDCQVDIAFPATQNEIDEHDAELLIKHGC 420
QY 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTQNRMSLNTWTRREVRD 480
DB 421 QYVEGAMPSSTNEAIHKYNKAGIICPGKANAAGVAVSGLEMTQNRMSLNTWTRREVRD 480
QY 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANITAGFTKVADAVAKGAV 526
DB 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANITAGFTKVADAVAKGAV 526

RESULT 3
ADQ36707 standard; protein; 526 AA.

ADQ36707;
XX

DT 23-SEP-2004 (first entry)
 XX NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.
 DE NADP-specific GDH alpha subunit precursor protein, SEQ ID 2.
 XX Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
 KW alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
 XX Chlorella sorokiniana.
 XX US2004128710-A1.
 XX
 XX 01-JUL-2004.
 XX
 XX 24-JUL-2003; 2003US-00627886.
 XX
 XX 01-MAY-1998; 98US-00070844.
 XX
 XX (SCHMIDT R R.
 XX (MILLER P.
 XX
 XX Schmidt RR, Miller P;
 XX
 XX WPI; 2004-533134/51.
 XX
 XX N-PSDB; ADQ36706.
 XX
 XX
 XX Increasing or decreasing nitrogen metabolism in plant cells, for plant
 PT with increased yield and improved tolerance to ammonia toxicity and
 PT osmotic stress, by transforming plant cell with nucleic acid having
 PT glutamate dehydrogenase activity.
 XX
 XX
 XX Claim 7; SEQ ID NO 2; 36pp; English.
 XX
 XX The present invention relates to increasing or decreasing the nitrogen
 CC metabolism in plant cells by transforming a plant cell with a
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
 CC ADQ36731), or their fragments, which exhibits GDH activity. The
 CC polynucleotide is operably linked to a polynucleotide encoding a
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
 CC fragments that exhibit chloroplast transit activity. The method is useful
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The
 CC methods, polynucleotides, and polypeptides are useful in producing plant
 CC with increased yield, and with improved tolerance to ammonia toxicity,
 CC osmotic stress, and composition of the crop or plant. The present
 CC sequence is the precursor protein of the alpha subunit of the NADP-
 CC specific GDH, which is then processed to produce the mature alpha subunit
 CC of the NADP-specific GDH, used in the method of the invention.
 CC
 XX
 XX Sequence 526 AA;
 SQ
 Query Match 100.0%; Score 2720; DB 8; Length 526;
 Best Local Similarity 100.0%; Pred. No. 1.3e-250;
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 VPAGDIGVAREIGYLFQGYKRITKNYTVLTPKQEGVSGSEIRPEATGYAVLFEVENVL 300
 QY 301 KDKGESLKGRCCLVSGAGNNAQVCAELLELEGALVLSLSSQGVYEPNGFTREQLQAVQ 360
 DB 301 KDKGESLKGRCCLVSGAGNNAQVCAELLELEGALVLSLSSQGVYEPNGFTREQLQAVQ 360
 QY 361 DMKKNSARISEKSTDAVYVGRKRPWELDCQVDIAPCATONEIDEHDAELLIKHCQ 420
 DB 361 DMKKNSARISEKSTDAVYVGRKRPWELDCQVDIAPCATONEIDEHDAELLIKHCQ 420
 QY 421 QYVEGANMPSTNAIHKYNKAGIYCPRKAANAGVAVSGLEMTQNRMSLMTREVERD 480
 DB 421 QYVEGANMPSTNAIHKYNKAGIYCPRKAANAGVAVSGLEMTQNRMSLMTREVERD 480
 QY 481 KLERIMDIYDSAMGSPRRYVNDLAAGANLAGFTKADAYKAQCAV 526
 DB 481 KLERIMDIYDSAMGSPRRYVNDLAAGANLAGFTKADAYKAQCAV 526
 RESULT 4
 ID AAM15408 standard; protein; 512 AA.
 XX AAM15408;
 AC AAM15408;
 XX
 DT 17-OCT-2003 (revised)
 DT 10-JUL-1997 (first entry)
 XX
 XX NADP-specific glutamate dehydrogenase beta-subunit precursor.
 DE
 XX Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
 KW chloroplast; transgenic plant.
 XX
 XX Chlorella sorokiniana; strain UTEX 1230.
 OS
 XX MO9712983-A1.
 XX
 XX 10-APR-1997.
 PD
 XX 03-OCT-1996; 96WO-US015921.
 XX
 XX 06-OCT-1995; 95US-00541033.
 XX
 XX (UYFL) UNIV FLORIDA.
 PA
 XX Schmidt RR, Miller P;
 PI
 XX WPI; 1997-226226/20.
 DR N-PSDB; AAT64530, AAT64543.
 XX
 XX DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
 PT plant cells.
 XX
 XX Claim 1; Page 29-32; 61pp; English.
 XX
 XX 2 Polypeptides (AAM15407 and AAM15408) respectively comprise the alpha
 CC (AAM15407) and beta subunit (AAM15408) precursor proteins of an ammonium-
 CC inducible, chloroplast-localised NADP-specific glutamate dehydrogenase
 CC (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha
 CC and beta subunits (see also AAM15411-12) that comprise the active NADP-
 CC GDH hexameric isoenzymes. The N metabolism of plants can be modulated
 CC (pref. increasing the assimilation of inorganic N into organic N) by
 CC transforming them with nucleotide sequences (see also AAT64529-30,
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
 CC proteins. Such plants show improved properties, e.g. increased crop yield
 CC and improved stress tolerance. Heterochimers having alpha and beta
 CC subunits can be expressed that have higher aminating/deaminating activity
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 XX Sequence 512 AA;
 SQ

Query Match 96.4%; Score 2621; DB 2; Length 512;
Best Local Similarity 97.3%; Pred. No. 3.6e-241;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MGTALVAKPIVAAPLAPRCLAPWPCAWRSARADRAKAVSLLEQISAMDATTTGDTA 60
DB 1 MGTALVAKPIVA-----CAWRSARADRAKAVSLLEQISAMDATTTGDTA 46

QY 61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120
DB 47 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 106

QY 121 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGFRVQSSAIGPYKGLRPHSVNL 180
DB 107 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGFRVQSSAIGPYKGLRPHSVNL 166

QY 181 SIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQSFMTLQRIHSYVD 240
DB 167 SIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQSFMTLQRIHSYVD 226

QY 241 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYGALFVENVL 300
DB 227 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYGALFVENVL 286

QY 301 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQ 360
DB 287 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQ 346

QY 361 DMKKKNSARISEKSDTAVYVGBRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGC 420
DB 347 DMKKKNSARISEKSDTAVYVGBRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGC 406

QY 421 QYVVEGANMPSSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLNTMTRREVRD 480
DB 407 QYVVEGANMPSSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLNTMTRREVRD 466

QY 481 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVAKAGAV 526
DB 467 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVAKAGAV 512

RESULT 5
AAU98951 standard; protein; 512 AA.

AC AAU98951;
XX
DT 24-SEP-2002 (first entry)
XX
DE NADP-glutamate dehydrogenase beta subunit.
XX
KW NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;
KM nitrogen metabolism; plant; ammonium assimilation; transgenic;
KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
OS Chlorella sorokiniana.
XX
FN US2002062495-A1.
XX
PD 23-MAY-2002.
XX
PE 01-MAY-1998; 98US-00070844.
XX
PR 01-MAY-1998; 98US-00070844.
XX
PA (SCHM/) SCHMIDT R R.
XX (MILL/) MILLER P.
XX
PI Schmidt RR, Miller P;
XX
DR WPI; 2002-499691/53.
XX N-PSDB; ABK51008.
XX

PT Transforming a plant with a polynucleotide encoding a polypeptide with
PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
PT metabolism useful to increase yield and ammonium and osmotic stress
PT tolerance.
XX
PS Claim 6; Page 17-18; 35pp; English.
XX
CC The invention relates to a method of modulating nitrogen metabolism in
CC plant cells, comprising transforming a plant cell with a polynucleotide
CC encoding a polypeptide having glutamate dehydrogenase activity, and
CC culturing the cell to produce descendant cells which express the
CC polypeptide. The method is used to provide plants with increased yield,
CC improved ammonium assimilation properties, increased tolerance to ammonia
CC toxicity, improved osmotic stress tolerance and improved composition. The
CC present sequence represents the amino acid sequence of Chlorella
CC sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method
CC of the invention
XX
SQ Sequence 512 AA.

Query Match 96.4%; Score 2621; DB 5; Length 512;
Best Local Similarity 97.3%; Pred. No. 3.6e-241;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MGTALVAKPIVAAPLAPRCLAPWPCAWRSARADRAKAVSLLEQISAMDATTTGDTA 60
DB 1 MGTALVAKPIVA-----CAWRSARADRAKAVSLLEQISAMDATTTGDTA 46

QY 61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 120
DB 47 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQOEPMQAVREAVSLQPVFEK 106

QY 121 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGFRVQSSAIGPYKGLRPHSVNL 180
DB 107 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGFRVQSSAIGPYKGLRPHSVNL 166

QY 181 SIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQSFMTLQRIHSYVD 240
DB 167 SIMKFLAFEQIFKNSLTTLPMGGGKGSDFDPKGSDAEVMRFQSFMTLQRIHSYVD 226

QY 241 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYGALFVENVL 300
DB 227 VPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGOEYGSSEIRPEATGYGALFVENVL 286

QY 301 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQ 360
DB 287 KDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQYVYEPNGFTREQLQAVQ 346

QY 361 DMKKKNSARISEKSDTAVYVGBRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGC 420
DB 347 DMKKKNSARISEKSDTAVYVGBRRKPELDCQVDIAFPQATONEIDEHDAELLIKHGC 406

QY 421 QYVVEGANMPSSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLNTMTRREVRD 480
DB 407 QYVVEGANMPSSTNEAIHKYNKAGIITPCGAANAGVAVSGLEMTONRMSLNTMTRREVRD 466

QY 481 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVAKAGAV 526
DB 467 KLERIMKDIYDSAMGSPSRRYNVDLAAGANIAGFTKVADAVAKAGAV 512

RESULT 6
ADQ36709 standard; protein; 512 AA.

AC ADQ36709;
XX
DT 23-SEP-2004 (first entry)
XX
DE NADP-specific GDH beta subunit precursor protein, SEQ ID 4.
XX
KW Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;
KM beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.
XX

XX Chlorella sorokiniana.
 OS US2004128710-A1.
 PN 01-JUL-2004.
 XX 24-JUL-2003; 2003US-00627886.
 XX 01-MAY-1998; 98US-00070844.
 PR (SCHM/) SCHMIDT R R.
 PA (MILL/) MILLER P.
 XX Schmidt RR, Miller P;
 PI WPI; 2004-533134/51.
 DR N-PSDB; ADQ36708.
 XX
 PT Increasing or decreasing nitrogen metabolism in plant cells, for plant
 PT with increased yield and improved tolerance to ammonia toxicity and
 PT osmotic stress, by transforming plant cell with nucleic acid having
 PT glutamate dehydrogenase activity.
 PS Claim 7; SEQ ID NO 4; 36pp; English.
 XX
 CC The present invention relates to increasing or decreasing the nitrogen
 CC metabolism in plant cells by transforming a plant cell with a
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
 CC ADQ36731), or their fragments, which exhibits GDH activity. The
 CC polynucleotide is operably linked to a polynucleotide encoding a
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
 CC fragments that exhibit chloroplast transit activity. The method is useful
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The
 CC methods, polynucleotides, and polypeptides are useful in producing plant
 CC with increased yield, and with improved tolerance to ammonia toxicity,
 CC osmotic stress, and composition of the crop or plant. The present
 CC sequence is the precursor protein of the beta subunit of the NADP-
 CC specific GDH, which is then processed to produce the mature alpha subunit
 CC of the NADP-specific GDH, used in the method of the invention.
 CC
 SQ Sequence 512 AA:
 Query Match 96.4%; Score 2621; DB 8; Length 512;
 Best Local Similarity 97.3%; Pred. No. 3.6e-241;
 Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MGTALVAKPIVAAAPLAPRCLAMPWRSARAKDVRAKVSLEBOISAMDATTTGPTA 60
 DB 1 MGTALVAKPIVAAAPLAPRCLAMPWRSARAKDVRAKVSLEBOISAMDATTTGPTA 46
 QY 61 LQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEOGEFNOAVREVAVSLOPYVEK 120
 DB 47 LQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEOGEFNOAVREVAVSLOPYVEK 106
 QY 121 RPPELLPFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
 DB 107 RPPELLPFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 166
 QY 181 SIMKFLAFEOIFKNSLTLLTPMGSGKSDPPKGSDAEVRFCOSFTELTQRIHSIYOD 240
 DB 167 SIMKFLAFEOIFKNSLTLLTPMGSGKSDPPKGSDAEVRFCOSFTELTQRIHSIYOD 226
 QY 241 VPADIGVAREIGLFGQYKRTKNTYGVLTLPKQEGSEIPEPATYGAIVFENVL 300
 DB 227 VPADIGVAREIGLFGQYKRTKNTYGVLTLPKQEGSEIPEPATYGAIVFENVL 286
 QY 301 KDKGESLKKRCLVSGAGNVAQYCAELLEKGAIVLISDSQGYVYEBNGFTRELOAVQ 360
 DB 287 KDKGESLKKRCLVSGAGNVAQYCAELLEKGAIVLISDSQGYVYEBNGFTRELOAVQ 346

QY 361 DMKKKNSARISEYKSDTAAYVVGDRRKPEWELCCOVDAIFPCATONEIDEHDAELLIKKQC 420
 DB 347 DMKKKNSARISEYKSDTAAYVVGDRRKPEWELCCOVDAIFPCATONEIDEHDAELLIKKQC 406
 QY 421 QYVEGANMPSTNEAIHKYNKAGIITCPGKAANGVAVSGLENTQNRMSLMTREBYRD 480
 DB 407 QYVEGANMPSTNEAIHKYNKAGIITCPGKAANGVAVSGLENTQNRMSLMTREBYRD 466
 QY 481 KLERIMKDIYDSAMGSPRRYVNDLAAGANITAGFTKVDAYVKAQGA 526
 DB 467 KLERIMKDIYDSAMGSPRRYVNDLAAGANITAGFTKVDAYVKAQGA 512

RESULT 7
 ID AAU98954 standard; protein; 487 AA.
 AC AAU98954;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Mature NADP-glutamate dehydrogenase alpha subunit.
 XX
 KW NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga;
 KW nitrogen metabolism; plant; ammonium assimilation; transgenic;
 KW ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
 XX
 OS Chlorella sorokiniana.
 OS US2002062495-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 01-MAY-1998; 98US-00070844.
 XX
 PR 01-MAY-1998; 98US-00070844.
 XX
 PA (SCHM/) SCHMIDT R R.
 PA (MILL/) MILLER P.
 PI Schmidt RR, Miller P;
 XX
 DR WPI; 2002-499691/53.
 DR N-PSDB; ABK51025.
 XX
 PT Transforming a plant with a polynucleotide encoding a polypeptide with
 PT glutamate dehydrogenase activity provides a plant with modulated nitrogen
 PT metabolism useful to increase yield and ammonium and osmotic stress
 PT tolerance.
 PS
 XX
 XX Claim 7; Page 27-28; 35pp; English.
 CC The invention relates to a method of modulating nitrogen metabolism in
 CC plant cells, comprising transforming a plant cell with a polynucleotide
 CC encoding a polypeptide having glutamate dehydrogenase activity, and
 CC culturing the cell to produce descendant cells which express the
 CC polypeptide. The method is used to provide plants with increased yield,
 CC improved ammonium assimilation properties, increased tolerance to ammonia
 CC toxicity, improved osmotic stress tolerance, and improved composition. The
 CC present sequence represents the amino acid sequence of Chlorella
 CC sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in
 CC the method of the invention
 CC
 SQ Sequence 487 AA:
 Query Match 92.2%; Score 2508; DB 5; Length 487;
 Best Local Similarity 100.0%; Pred. No. 2.1e-230;
 Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AVSLEBOISAMDATTTGPTALQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEQ 100
 DB 2 AVSLEBOISAMDATTTGPTALQKAVKQMATKAGTEGLVHGIKNPDVROLLEIFMKDPEQ 61

Qy	101	QEQMAVREAVSLQVFEKRPDLPIFKQIVTEPRVITFPVSVLDDAGNQLQVNRGRVQ	160
Dd	62	QEEQMAAREAVASLQVFEKRPDLPIFKQIVTEPRVITFPVSVLDDAGNQLQVNRGRVQ	121
Qy	161	YSSAIGPYKGLRFHPSPVNLISMKFLAFEQIPKNSLITLPMGGGKGSGSDFPKGSDAEV	220
Dd	122	YSSAIGPYKGLRFHPSPVNLISMKFLAFEQIPKNSLITLPMGGGKGSGSDFPKGSDAEV	181
Qy	221	MRFQSFMTLQHHISYVDVPAQDVGUGAREIGYLFQGYKRIITKNYTGVLTPKGOEYGG	280
Dd	182	MRFQSFMTLQHHISYVDVPAQDVGUGAREIGYLFQGYKRIITKNYTGVLTPKGOEYGG	241
Qy	281	SEIRPEPTGGAULFPENTLKDKGESLKKRCLVSGAGNVAYQCAELLLEKALIVSLSD	340
Dd	242	SEIRPEPTGGAULFPENTLKDKGESLKKRCLVSGAGNVAYQCAELLLEKALIVSLSD	301
Qy	341	SGQVYVEPNQFTREQQAVQDMKKKNSARISEYSDTPAVYVYGDPRKRWELDDCCVDIAFP	400
Dd	302	SGQVYVEPNQFTREQQAVQDMKKKNSARISEYSDTPAVYVYGDPRKRWELDDCCVDIAFP	361
Qy	461	GLEMTQNRMSLMTREVPDKLERIMKDIYDSAMGPSRRYVNDLAAGANITAGFTKADAV	520
Dd	422	GLEMTQNRMSLMTREVPDKLERIMKDIYDSAMGPSRRYVNDLAAGANITAGFTKADAV	481
Qy	521	KAQGAV 526	
Dd	482	KAQGAV 487	
RESULT 8			
AC	ADQ36729	standard; protein; 487 AA.	
XX	ADQ36729;		
AC	ADQ36729;		
XX	ADQ36729;		
DT	23-SEP-2004	(first entry)	
XX			
DE		Mature NADP-specific GDH alpha subunit, SEQ ID 24.	
XX			
KW		Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;	
XX		alpha subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.	
OS		Chlorella sorokiniana.	
XX			
PN	US2004128710-A1.		
XX			
PD	01-JUL-2004.		
XX			
PF	24-JUL-2003; 2003US-00627886.		
XX			
ER	01-MAY-1998; 98US-00070844.		
XX			
PA	(SCHM//) SCHMIDT R. R.		
PA	(MILL//) MILLER P.		
XX			
PI	Schmidt RR, Miller P;		
XX			
WI	WPI; 2004-533134/51.		
DR	N-PSDB; ADQ36728.		
XX			
PT		Increasing or decreasing nitrogen metabolism in plant cells, for plant	
XX		with increased yield and improved tolerance to ammonia toxicity and	
PT		osmotic stress, by transforming plant cell with nucleic acid having	
PT		glutamate dehydrogenase activity.	
XX			
PS	Claim 7; SEQ ID NO 24; 36pp; English.		
XX			
CC		The present invention relates to increasing or decreasing the nitrogen	
CC		metabolism in plant cells by transforming a plant cell with a	

CC		polynucleotide encoding a polypeptide having glutamate dehydrogenase
CC	(GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH	
CC	(ADG36709, ADG36729), a beta subunit of NADP-specific GDH (ADQ36709,	
CC	ADQ36731), or their fragments, which exhibits GDH activity. The	
CC	polynucleotide is operably linked to a polynucleotide encoding a	
CC	chloroplast transit peptide comprising ADQ36710 or ADQ36731, or their	
CC	fragments that exhibit chloroplast transit activity. The method is useful	
CC	for increasing or decreasing the nitrogen metabolism in plant cells. The	
CC	methods, polynucleotides, and with improved tolerance to ammonia toxicity,	
CC	with increased yield, and composition of the crop or plant. The present	
CC	osmotic stress, and composition of the crop or plant. The present	
CC	sequence is the mature alpha subunit of the NADP-specific GDH used in the	
CC	method of the invention.	
XX		
SQ	Sequence 487 AA;	
	Query Match 92.2%; Score 2508; DB 8; Length 487;	
	Best Local Similarity 100.0%; Pred. No. 2,1e-230;	
	Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	41 AVSLSEEOISAMDATGTGFALOKAVKONATKAGTEGLVHGINKDPVRQLLIEIPMKDPEQ	100
DB	2 AVLSLEEQISAMDATGTGFALOKAVKONATKAGTEGLVHGINKDPVRQLLIEIPMKDPEQ	61
OY	101 QEFMOVAEVAVSLOPVFEKPPELLPIRKQIVPERVITFRWSWLDNNGNLFRRQ	160
DB	62 QEFMOVAEVAVSLOPVFEKPPELLPIRKQIVPERVITFRWSWLDNNGNLFRRQ	121
OY	161 YSSAIGPKFGGRFPFSPYNLSIMKFLAEQIFKNSLTTLPMGGKGSGDFDPKGSDAEV	220
DB	122 YSSAIGPKFGGRFPFSPYNLSIMKFLAEQIFKNSLTTLPMGGKGSGDFDPKGSDAEV	181
OY	221 MRFCQSFMTELQRHSIYQDVPAVDIGVAREIGYLPFOYKRITKNYTGVLTTPKQERYCG	280
DB	182 MRFCQSFMTELQRHSIYQDVPAVDIGVAREIGYLPFOYKRITKNYTGVLTTPKQERYCG	241
OY	281 SEIRPEARAGXAVLVENVLLDKGSLTKGKRLTVSAGNVAYCAELLEKGAIVLSLD	340
DB	242 SEIRPEARAGXAVLVENVLLDKGSLTKGKRLTVSAGNVAYCAELLEKGAIVLSLD	301
OY	341 SGGYYEEENGFTREOLQAVODMKKKNNGARISEYSPTAVVYGDRRKPWELDCQVDIAFP	400
DB	302 SGGYYEEENGFTREOLQAVODMKKKNNGARISEYSPTAVVYGDRRKPWELDCQVDIAFP	361
OY	401 CATONEIDEHDAELLIKHCQYVVEGANMPSITNEAIHKYKXAGITYCPGKAANAGVAVS	460
DB	362 CATONEIDEHDAELLIKHCQYVVEGANMPSITNEAIHKYKXAGITYCPGKAANAGVAVS	421
OY	461 GLEMTQNMSLWNTREEVRDKLERIMKOIYDSAMPSSRYNDLAAGANIAGFTKYADV	520
DB	422 GLEMTQNMSLWNTREEVRDKLERIMKOIYDSAMPSSRYNDLAAGANIAGFTKYADV	481
OY	521 KAQGAV 526	
DB	482 KAQGAV 487	
<hr/>		
RESULT 9		
AAW15411		
ID	AAW15411 standard; protein; 487 AA.	
XX	AAW15411;	
AC	17-OCT-2003 (revised)	
XX	10-JUL-1997 (first entry)	
DT	NADP-specific glutamate dehydrogenase alpha subunit.	
XX	Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;	
KW	chloroplast; transgenic plant.	
XX	Chlorella sorokiniana; strain UTEX 1330.	
OS		

PN W09712983-A1.
 XX
 PD 10-APR-1997.
 XX
 PF 03-OCT-1996; 96WO-US015921.
 XX
 PR 06-OCT-1995; 95US-00541033.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Schmidt RR, Miller P;
 XX
 DR WPI: 1997-226226/20.
 DR N-PSDB; AAT64547.
 XX
 PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
 PT plant cells.
 XX
 PS Claim 1; Page 44-46; 61pp; English.
 XX
 CC 2. Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
 CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
 CC ammonium-inducible, chloroplast-localised hexameric NADP-specific
 CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
 CC They are produced by removal of transit peptides from the precursor
 CC proteins (AAW15407-08). The N metabolism of plants can be modulated
 CC (pref. increasing the assimilation of inorganic N into organic N) by
 CC transforming them with nucleotide sequences (see also AAT64529-30,
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
 CC proteins. Such plants show improved properties, e.g. increased crop yield
 CC and improved stress tolerance. Heterohexamers having alpha and beta
 CC subunits can be expressed that have higher aminating/deaminating activity
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 487 AA:
 Query Match 91.9%; Score 2500; DB 2; Length 487;
 Best Local Similarity 99.8%; Pred. No. 1.2e-229;
 Matches 485; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 41 AVSLSEEDISAMDTGDFTLQKAVKQMATKATGEGVHGIKNPDVRLTLTEIFMKDEQ 100
 DB 2 AVSLSEEDISAMDTGDFTLQKAVKQMATKATGEGVHGIKNPDVRLTLTEIFMKDEQ 61
 QY 101 QEFMQAVREAVNSIQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 160
 DB 62 QEFMQAVREAVNSIQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQ 121
 QY 161 YSSAIGPYKGGLRHPSPVNSIMKFLAEQIFKNSLTLPMGGGKGSDDPKGKSDAEV 220
 DB 122 YSSAIGPYKGGLRHPSPVNSIMKFLAEQIFKNSLTLPMGGGKGSDDPKGKSDAEV 181
 QY 221 MRFCQSMTELORHHSYVDVPADIGVAREIGTLFCQYRIRTKNTYGLVTPKGQEVG 280
 DB 182 MRFCQSMTELORHHSYVDVPADIGVAREIGTLFCQYRIRTKNTYGLVTPKGQEVG 241
 QY 281 SEIRPEATGYAVFVENVLKDKGESLKGKCLVSGAGNVAQCAELLLEKGAIVLSLD 340
 DB 242 SEIRPEATGYAVFVENVLKDKGESLKGKCLVSGAGNVAQCAELLLEKGAIVLSLD 301
 QY 341 SQGYVYEPNGFTREBQLOAVQDMKKKNSARISEYKSDTAVYVGRRKPEWLDCCVDIAFP 400
 DB 302 SQGYVYEPNGFTREBQLOAVQDMKKKNSARISEYKSDTAVYVGRRKPEWLDCCVDIAFP 361
 QY 401 CATONEIDEHDAELLIKHGCGVYVVGAMBPSTNAIHKYNKAGITTCGKAAANGAVVS 460
 DB 362 CATONEIDEHDAELLIKHGCGVYVVGAMBPSTNAIHKYNKAGITTCGKAAANGAVVS 421
 QY 461 GLENTQNRMSLAWTREVVDKLERIMKDIYSAMGSPRRYVNDLAAGANIGFTKVDAY 520
 DB 422 GLENTQNRMSLAWTREVVDKLERIMKDIYSAMGSPRRYVNDLAAGANIGFTKVDAY 481

QY 521 KAOGAV 526
 DB 482 KAOGAV 487
 RESULT 10
 AAW15412
 ID AAW15412 standard; protein; 476 AA.
 XX
 AC AAW15412;
 XX
 DT 17-OCT-2003 (revised)
 DT 10-JUL-1997 (first entry)
 XX
 DE NADP-specific glutamate dehydrogenase beta subunit.
 XX
 KW Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
 KW chloroplast; transgenic plant.
 OS Chlorella sorokiniana; strain UTEX 1230.
 XX
 OS W09712983-A1.
 XX
 PD 10-APR-1997.
 XX
 PF 03-OCT-1996; 96WO-US015921.
 XX
 PR 06-OCT-1995; 95US-00541033.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Schmidt RR, Miller P;
 XX
 DR WPI: 1997-226226/20.
 DR N-PSDB; AAT64548.
 XX
 PT DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella
 PT sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
 PT plant cells.
 XX
 PS Claim 1; Page 48-50; 61pp; English.
 XX
 CC 2. Polypeptides (AAW15411 and AAW15412) respectively comprise the mature
 CC alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an
 CC ammonium-inducible, chloroplast-localised hexameric NADP-specific
 CC glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
 CC They are produced by removal of transit peptides from the precursor
 CC proteins (AAW15407-08). The N metabolism of plants can be modulated
 CC (pref. increasing the assimilation of inorganic N into organic N) by
 CC transforming them with nucleotide sequences (see also AAT64529-30,
 CC AAT64547-48) encoding the alpha and/or beta subunits or precursor
 CC proteins. Such plants show improved properties, e.g. increased crop yield
 CC and improved stress tolerance. Heterohexamers having alpha and beta
 CC subunits can be expressed that have higher aminating/deaminating activity
 CC ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 476 AA:
 Query Match 90.6%; Score 2465; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.7e-226;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 MDATTGDFTLQKAVKQMATKATGEGVHGIKNPDVRLTLTEIFMKDEQEFMQAVREV 110
 DB 1 MDATTGDFTLQKAVKQMATKATGEGVHGIKNPDVRLTLTEIFMKDEQEFMQAVREV 60
 QY 111 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVYSSAIGPYK 170
 DB 61 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVYSSAIGPYK 120
 QY 171 GLRHPSPVNSIMKFLAEQIFKNSLTLPMGGGKGSDDPKGKSDAEVNRFCQSMTE 230

Db 121 GLRHPSPVNSIMKFLAEQIFKNSLTTLPMWGGKGSDDPKGKSDAEVWRFQSPFTE 180
Qy 231 LQHHISYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 290
Db 181 LQHHISYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 240
Qy 291 GAVLFVENVLKDKGESLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVEPENG 350
Db 241 GAVLFVENVLKDKGESLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVEPENG 300
Qy 351 FTREQLQAVODMKKNNNSARISEKSDTAVYVGDRRKPELDCQVDIAFPATONEIDEH 410
Db 301 FTREQLQAVODMKKNNNSARISEKSDTAVYVGDRRKPELDCQVDIAFPATONEIDEH 360
Qy 411 DAELLIRHGCQYVEGANMPESTNEAIIHKYNKAGIITCGKAAANGVAVSGLEWTQNRMS 470
Db 361 DAELLIRHGCQYVEGANMPESTNEAIIHKYNKAGIITCGKAAANGVAVSGLEWTQNRMS 420
Qy 471 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVA DAVAKAGAV 526
Db 421 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVA DAVAKAGAV 476

RESULT 11
AAU98955 standard; protein; 476 AA.

AAU98955;

24-SEP-2002 (first entry)

Mature NADP-glutamate dehydrogenase beta subunit.

NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; alga;
nitrogen metabolism; plant; ammonium assimilation; transgenic;
ammonia toxicity tolerance; osmotic stress tolerance; enzyme.

Chlorella sorokiniana.

US2002062495-A1.

23-MAY-2002.

01-MAY-1998; 98US-00070844.

01-MAY-1998; 98US-00070844.

(SCHM/) SCHMIDT R R.

(MILL/) MILLER P.

Schmidt RR, Miller P;

WPI; 2002-499691/53.

N-PSDB; ABK51026.

Transforming a plant with a polynucleotide encoding a polypeptide with
glutamate dehydrogenase activity provides a plant with modulated nitrogen
metabolism useful to increase yield and ammonium and osmotic stress
tolerance.

Claim 7; Page 31-32; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in
plant cells, comprising transforming a plant cell with a polynucleotide
encoding a polypeptide having glutamate dehydrogenase activity, and
culturing the cell to produce descendant cells which express the
polypeptide. The method is used to provide plants with increased yield,
improved ammonium assimilation properties, increased tolerance to ammonia
toxicity, improved osmotic stress tolerance and improved competition. The
present sequence represents the amino acid sequence of Chlorella
sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the
method of the invention

XX Sequence 476 AA;

Query Match 90.6%; Score 2465; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 2.7e-226;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 MDATTGDFTLQAVKMATKAGTEGLVHGIKNPDVRLQTLTELFMKDPEQDEFMAQVREV 110
Db 1 MDATTGDFTLQAVKMATKAGTEGLVHGIKNPDVRLQTLTELFMKDPEQDEFMAQVREV 60

Qy 111 AVSLQPVFEKRPPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGRVQSSAIGPYKG 170
Db 61 AVSLQPVFEKRPPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGRVQSSAIGPYKG 120

Qy 171 GLRHPSPVNSIMKFLAEQIFKNSLTTLPMWGGKGSDDPKGKSDAEVWRFQSPFTE 230
Db 121 GLRHPSPVNSIMKFLAEQIFKNSLTTLPMWGGKGSDDPKGKSDAEVWRFQSPFTE 180

Qy 231 LQHHISYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 290
Db 181 LQHHISYVQDVPAGDIGVAREIGYLFQYKRIITKNYTGVLTPKGQYGGSEIRPEATGY 240

Qy 291 GAVLFVENVLKDKGESLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVEPENG 350
Db 241 GAVLFVENVLKDKGESLKGRCLVSGAGNVAQYCAELLLEKGAIVLSLSQGYVEPENG 300

Qy 351 FTREQLQAVODMKKNNNSARISEKSDTAVYVGDRRKPELDCQVDIAFPATONEIDEH 410
Db 301 FTREQLQAVODMKKNNNSARISEKSDTAVYVGDRRKPELDCQVDIAFPATONEIDEH 360

Qy 411 DAELLIRHGCQYVEGANMPESTNEAIIHKYNKAGIITCGKAAANGVAVSGLEWTQNRMS 470
Db 361 DAELLIRHGCQYVEGANMPESTNEAIIHKYNKAGIITCGKAAANGVAVSGLEWTQNRMS 420

Qy 471 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVA DAVAKAGAV 526
Db 421 LNMTRREVRDKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVA DAVAKAGAV 476

RESULT 12

ADQ36731 standard; protein; 476 AA.

ADQ36731;

23-SEP-2004 (first entry)

Mature NADP-specific GDH beta subunit, SEQ ID 26.

Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; enzyme;

beta subunit; NADP-specific GDH; NADP-specific glutamate dehydrogenase.

Chlorella sorokiniana.

US2004128710-A1.

01-JUL-2004.

24-JUL-2003; 2003US-00627886.

01-MAY-1998; 98US-00070844.

(SCHM/) SCHMIDT R R.

(MILL/) MILLER P.

Schmidt RR, Miller P;

WPI; 2004-53134/51.

N-PSDB; ADQ36730.

Increasing or decreasing nitrogen metabolism in plant cells, for plant
with increased yield and improved tolerance to ammonia toxicity and

PT osmotic stress, by transforming plant cell with nucleic acid having
 PT glutamate dehydrogenase activity.
 XX
 PS Claim 7; SEQ ID NO 26; 366p; English.
 XX
 CC The present invention relates to increasing or decreasing the nitrogen
 CC metabolism in plant cells by transforming a plant cell with a
 CC polynucleotide encoding a polypeptide having glutamate dehydrogenase
 CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH
 CC (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709,
 CC ADQ36731), or their fragments, which exhibits GDH activity. The
 CC polynucleotide is operably linked to a polynucleotide encoding a
 CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their
 CC fragments that exhibit chloroplast transit activity. The method is useful
 CC for increasing or decreasing the nitrogen metabolism in plant cells. The
 CC methods, polynucleotides, and polypeptides are useful in producing plant
 CC with increased yield, and with improved tolerance to ammonia toxicity,
 CC osmotic stress, and composition of the crop or plant. The present
 CC sequence is the mature beta subunit of the NADP-specific GDH used in the
 CC method of the invention.
 CC
 SQ Sequence 476 AA;
 Query Match 90.6%; Score 2465; DB 8; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2,7e-226;
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 MDATGTFPLAQAKVQKMATAGTEGLVHGKNDVRLTEIFMKDEQGEFQAVREV 110
 DB 1 MDATGTFPLAQAKVQKMATAGTEGLVHGKNDVRLTEIFMKDEQGEFQAVREV 60
 QY 111 AVSIQPVPEKRELPPIFKQIVPEPRTFRVSWLDDGNGVNRGPRVQSSAIGPKG 170
 DB 61 AVSIQPVPEKRELPPIFKQIVPEPRTFRVSWLDDGNGVNRGPRVQSSAIGPKG 120
 QY 171 GLRHPSEVNSIMKFLAEQIFKNSLTLLPMGGGSGSDPFGKSDAEVRFQOSFMT 230
 DB 121 GLRHPSEVNSIMKFLAEQIFKNSLTLLPMGGGSGSDPFGKSDAEVRFQOSFMT 180
 QY 231 LQRIHSYVDVPADIGVAREIGYLFQGYRITKNTYGVLTLPKQEGSGSEIRPEATGY 290
 DB 181 LQRIHSYVDVPADIGVAREIGYLFQGYRITKNTYGVLTLPKQEGSGSEIRPEATGY 240
 QY 291 GAVLFVENVLKDKRESLKGRKCLVSGAGNVAQYCAELLLEGAIVLSLSDSQGYVEPBG 350
 DB 241 GAVLFVENVLKDKRESLKGRKCLVSGAGNVAQYCAELLLEGAIVLSLSDSQGYVEPBG 300
 QY 351 FTREQLAVQDMKKKNSARISEYKSDTAVVYGDRRKPMELDCOVDAFPCATONEIDEH 410
 DB 301 FTREQLAVQDMKKKNSARISEYKSDTAVVYGDRRKPMELDCOVDAFPCATONEIDEH 360
 QY 411 DAEILLRHGCGYVEGANGMPSTNEAIHKYKAGIITCYGKAANGVAVASGLEMTONRMS 470
 DB 361 DAEILLRHGCGYVEGANGMPSTNEAIHKYKAGIITCYGKAANGVAVASGLEMTONRMS 420
 QY 471 LMTREVRDLGLEIMDIYDSAMGPRRRVNDLAAGNINIGFTKVADAVAAQAGAV 526
 DB 421 LMTREVRDLGLEIMDIYDSAMGPRRRVNDLAAGNINIGFTKVADAVAAQAGAV 476

RESULT 13

ABU38763
 ID ABU38763 standard; protein, 445 AA.
 XX
 AC ABU38763;
 DT 19-JUN-2003 (first entry)
 DB Protein encoded by prokaryotic essential gene #24290.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Pseudomonas aeruginosa.

XX
 PN W0200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA42633.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 66687; 1766p; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 445 AA;
 Query Match 48.1%; Score 1309; DB 6; Length 445;
 Best Local Similarity 59.2%; Pred. No. 9.3e-116;
 Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
 QY 86 VROLTEIFMKDPQGEFQAVREAVASLQVPEKRELP--IFKQIVPEPRTFRV 143
 DB 5 VDAFLERLKRDPQGEFQAVREAVASLQVPEKRELP--IFKQIVPEPRTFRV 64
 QY 144 WLDDAGNLQVNRGPRVQSSAIGPKGGLRHPSEVNSIMKFLAEQIFKNSLTLLPMGG 203
 DB 65 WVDQGRVVRNVRGPRVQSSAIGPKGGLRHPSEVNSIMKFLAEQIFKNSLTLLPMGG 124

DR WPI: 2004-420615/39.

XX New compositions having outer-membrane vesicles and proteins from
PT *Neisseria meningitidis*, useful in the field of meningococcal
PT biochemistry, in particular for preventing and/or treating meningococcal
PT infections.

PS Claim 9; SEQ ID NO 163; 79pp; English.

XX
XX
CC The invention relates to a novel composition comprising outer-membrane
CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and
CC 1 or more proteins which are present in OMVs prepared from a second
CC strain of *N. meningitidis*, but which are not present in OMVs prepared
CC from the first strain. The composition of the invention demonstrates
CC antibacterial and anti-inflammatory activities and may be useful in the
CC field of meningococcal biochemistry, in particular the trafficking and
CC localisation of meningococcal proteins, as well as in the prevention or
CC treatment of meningococcal infections, possibly via the production of a
CC vaccine or gene therapy. The current sequence is that of a *Neisseria*
CC *meningitidis* MCS8 outer-membrane vesicle (OMV)-related membrane protein
CC of the invention.

SQ Sequence 444 AA;

Query Match 47.8%; Score 1300.5; DB 8; Length 444;
Best Local Similarity 57.4%; Pred. No. 66-115;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;

QY 85 DVRLQLTEIFMKDEBQEFMQAVREAVASIQPFKEKPELL--PIFKQIVPERVITFRV 142
DB 3 DLNTLFLANLKKRNPNQSEPFHQAVEVEFMSLDPLAKNPKYQOSLIERIVEPERVIMFRV 62
QY 143 SWLDDAGNLQVNRGRFRVQYSSAIGPYKGLRFPSPVNLSTIMKFLAFEOIFKNSLITLPMG 202
DB 63 TWODDKQOVQVNRGRFRVQYSSAIGPYKGLRFPSPVNLSTIMKFLAFEOIFKNSLITLPMG 122
QY 203 GKGSGSPDFDPKSGDAEVMRFQSPFMTLORHISYVODVPAGDIGVGAREIGYLFQGYKR 262
DB 123 GKGSGSPDFDPKSGDAEVMRFQSPFMTLORHISYVODVPAGDIGVGAREIGYLFQGYKR 182
QY 263 ITKNYTVLTPKGOEYGGSEIRPEATGYAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 322
DB 183 IRNPFSSVLTKGLEWGSGLIRPEATGYAVLFVENVLKDKGSLKGRCLVSGAGNVAQ 242
QY 323 YCAELLLEKGAIVLSDSQGYTER--NGFTREQLQAVQDKKKNSARISEYKSDTAVY 381
DB 243 YAAEKAIQLGAKVLTVSDSNGLVLPDSCMTQALAILIEKVRRE--RVATYAKEOGLQ 301
QY 382 VGDRRKPEMLDCCQVDIAPCATONEIDEHDAELLIKGCOYVVEGANNPSTNEAIHKYK 441
DB 302 YFEKQKPMGV--AAEIALPCATONEIDEHDAELLIKGCOYVVEGANNPSTLGAVEQFIK 359
QY 442 AGIITYCPKAAAGVAVSGLMTQNRMSLNTREBYVDKLERIMKDIYDSAGMPSRRY- 500
DB 360 AGIITYAPGKASNAGVATSGLEMSQNAIRLSMTREBYDQRLFGIMOSIHESCL----KYG 415
QY 501 ----NVDLAAGANIAGFTKVAADAVKAQ 524
DB 416 KVGDTVYVYNGANIGAVKADAMLAQ 443

Search completed: July 9, 2005, 18:32:04
Job time: 174 secs

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OM protein - protein search, using SW model

Run on: July 9, 2005, 18:26:33 ; Search time 43 Seconds

(without alignments)
913.149 Million cell updates/sec

Title: US-10-627-886-2

Perfect score: 2720
Sequence: 1 MOTALVAKPIVAAPLAARPR.....GANIAGFTKVAADAVKAGAV 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2720	100.0	526	2	US-08-541-033A-2
2	2720	100.0	526	2	US-08-828-451-2
3	2621	96.4	512	2	US-08-541-033A-4
4	2621	96.4	512	2	US-08-828-451-4
5	2508	92.2	487	2	US-08-541-033A-24
6	2508	92.2	487	2	US-08-828-451-24
7	2465	90.6	476	2	US-08-541-033A-26
8	2465	90.6	476	2	US-08-828-451-26
9	1309	48.1	450	4	US-09-252-991A-20646
10	1257.5	46.2	467	4	US-09-328-352-5725
11	1234.5	45.4	448	4	US-09-134-000C-3884
12	1221	44.9	448	4	US-09-583-110-4489
13	1201	44.2	447	2	US-08-886-640-3
14	1201	44.2	447	3	US-08-884-235-11
15	1200	44.1	447	1	US-08-370-193A-11
16	1191	43.8	452	4	US-09-489-039A-7937
17	1177.5	43.3	446	4	US-09-543-681A-6657
18	1177	43.3	447	3	US-08-508-761B-6
19	1147	42.2	461	3	US-09-171-337A-5
20	1147	42.2	461	4	US-09-631-022-5
21	1143	42.0	454	1	US-08-831-753-1
22	1037.5	38.1	454	4	US-09-538-092-767
23	1012	37.2	368	4	US-09-107-433-4041
24	788.5	29.0	298	4	US-09-248-796A-17483
25	552.5	20.3	420	3	US-09-134-001C-3103
26	537.5	19.8	374	4	US-09-710-279-2162
27	537	19.7	509	4	US-09-902-540-11352

28	519	19.1	420	3	US-09-239-303-9	Sequence 9, Appli
29	482.5	17.7	409	4	US-09-902-540-12638	Sequence 12638, A
30	476.5	17.5	421	3	US-09-239-303-2	Sequence 2, Appli
31	458.5	16.9	427	4	US-09-328-352-6130	Sequence 6130, Ap
32	441	16.2	432	4	US-09-489-039A-13935	Sequence 13935, A
33	385	14.2	87	2	US-08-461-990B-22	Sequence 20, Appl
34	368	13.5	87	2	US-08-461-990B-20	Sequence 20, Appl
35	364.5	13.4	558	4	US-09-538-092-1153	Sequence 1153, Ap
36	357	13.1	87	2	US-08-461-990B-23	Sequence 23, Appl
37	357	13.1	558	4	US-09-538-092-832	Sequence 832, App
38	357	13.1	575	4	US-09-949-016-7622	Sequence 7622, Ap
39	357	13.1	575	4	US-09-949-016-7623	Sequence 7623, Ap
40	346	12.7	176	4	US-09-248-796A-17482	Sequence 17482, A
41	168	6.2	87	2	US-08-461-990B-21	Sequence 21, Appl
42	157.5	5.8	366	2	US-08-804-689-2	Sequence 2, Appli
43	139.5	5.1	356	2	US-08-461-990B-2	Sequence 122, App
44	138	5.1	1092	4	US-09-538-092-122	Sequence 991, App
45	131	4.8	351	4	US-09-198-452A-991	

ALIGNMENTS

RESULT 1

US-08-541-033A-2

Sequence 2, Application US/08541033A

Patent No. 5879941

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Saliwanichik & Saliwanichik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,033A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: UP155

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 375-8100

TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 526 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-541-033A-2

Query Match 100.0%; Score 2720; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 7.6e-243;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVAAPLAARPRCLAPWPCAWRSARADVRARAVSLSEQISAMDATGDFTA 60
DB 1 MOTALVAKPIVAAPLAARPRCLAPWPCAWRSARADVRARAVSLSEQISAMDATGDFTA 60

QY 61 LOKAVKOMATKATGEGVHGIKNPDVRLTEIFMKDPEQOEFMQAVREAVSLQPFEEK 120
DB 61 LOKAVKOMATKATGEGVHGIKNPDVRLTEIFMKDPEQOEFMQAVREAVSLQPFEEK 120
QY 121 RPELLPIFKQIVPERVITFRVSWLDDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
DB 121 RPELLPIFKQIVPERVITFRVSWLDDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
QY 181 SIMKFLAFOEIFKNSLITLPMGGKGGSDPDPKGSDAEVNRFCQSFMTLQRIHSYVD 240
DB 181 SIMKFLAFOEIFKNSLITLPMGGKGGSDPDPKGSDAEVNRFCQSFMTLQRIHSYVD 240
QY 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKQEGYGSSEIRPEATGYAVLFVENVL 300
DB 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKQEGYGSSEIRPEATGYAVLFVENVL 300
QY 301 KDKGESLKGRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQ 360
DB 301 KDKGESLKGRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQ 360
QY 361 DMKKNNNSARISEKSDTAVYVGDRRKPMELDCQVDIAFPCATONEIDEHDAELLKHGC 420
DB 361 DMKKNNNSARISEKSDTAVYVGDRRKPMELDCQVDIAFPCATONEIDEHDAELLKHGC 420
QY 421 QYVEGANMSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLNTTREVVD 480
DB 421 QYVEGANMSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLNTTREVVD 480
QY 481 KLERIMDIYDSAMGPRSRRYVNDLAAGANIAGFTKVADAVKAGAV 526
DB 481 KLERIMDIYDSAMGPRSRRYVNDLAAGANIAGFTKVADAVKAGAV 526

RESULT 2

US-08-828-451-2
Sequence 2, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UFI155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-451-2

Query Match 100.0%; Score 2720; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 7,6e-243;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTALVAKPIVAAPLAPRCLAPMPCAMWRSKRDVRAKAVLEQISAMDATTGDFTA 60
DB 1 MOTALVAKPIVAAPLAPRCLAPMPCAMWRSKRDVRAKAVLEQISAMDATTGDFTA 60
QY 61 LOKAVKOMATKATGEGVHGIKNPDVRLTEIFMKDPEQOEFMQAVREAVSLQPFEEK 120
DB 61 LOKAVKOMATKATGEGVHGIKNPDVRLTEIFMKDPEQOEFMQAVREAVSLQPFEEK 120
QY 121 RPELLPIFKQIVPERVITFRVSWLDDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
DB 121 RPELLPIFKQIVPERVITFRVSWLDDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
QY 181 SIMKFLAFOEIFKNSLITLPMGGKGGSDPDPKGSDAEVNRFCQSFMTLQRIHSYVD 240
DB 181 SIMKFLAFOEIFKNSLITLPMGGKGGSDPDPKGSDAEVNRFCQSFMTLQRIHSYVD 240
QY 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKQEGYGSSEIRPEATGYAVLFVENVL 300
DB 241 VPAGDIGVAREIGYLFQGYKRIITKNYTGVLTPKQEGYGSSEIRPEATGYAVLFVENVL 300
QY 301 KDKGESLKGRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQ 360
DB 301 KDKGESLKGRCCLVSGAGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVQ 360
QY 361 DMKKNNNSARISEKSDTAVYVGDRRKPMELDCQVDIAFPCATONEIDEHDAELLKHGC 420
DB 361 DMKKNNNSARISEKSDTAVYVGDRRKPMELDCQVDIAFPCATONEIDEHDAELLKHGC 420
QY 421 QYVEGANMSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLNTTREVVD 480
DB 421 QYVEGANMSTNEAIHKYNKAGIIPCCKAANAGVAVSGLEMTQNRMSLNTTREVVD 480
QY 481 KLERIMDIYDSAMGPRSRRYVNDLAAGANIAGFTKVADAVKAGAV 526
DB 481 KLERIMDIYDSAMGPRSRRYVNDLAAGANIAGFTKVADAVKAGAV 526

RESULT 3

US-08-541-033A-4
Sequence 4, Application US/08541033A
Patent No. 5879941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-541-033A-4

Query Match 96.4%; Score 2621; DB 2; Length 512;
Best Local Similarity 97.3%; Pred. No. 1,1e-233;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTLVAKPIVAAPLAARPRCLAPWPCAWRSARVDRAKAVSLSEQISANDATTGDTA 60
DB 1 MOTLVAKPIVA-----CAWRSARVDRAKAVSLSEQISANDATTGDTA 46
QY 61 LQKAVKQMATKATGTEGLVHGINKPDPVROLTEIFMKDPEOEFMOAVREAVVSLQPVREK 120
DB 47 LQKAVKQMATKATGTEGLVHGINKPDPVROLTEIFMKDPEOEFMOAVREAVVSLQPVREK 106
QY 121 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
DB 107 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 166
QY 181 SIMFLAFEOIFKNSLTLLPMGGGKGSDFPKGSDAEVWRFQSFMTTELQRIHSYQD 240
DB 167 SIMFLAFEOIFKNSLTLLPMGGGKGSDFPKGSDAEVWRFQSFMTTELQRIHSYQD 226
QY 241 VPADIGVAREIGYLFQYKRIKNTYGVLTLPKQEGSGEIRPEATGVALFVENVL 300
DB 227 VPADIGVAREIGYLFQYKRIKNTYGVLTLPKQEGSGEIRPEATGVALFVENVL 286
QY 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNNGFTREQLQAVQ 360
DB 287 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNNGFTREQLQAVQ 346
QY 361 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCQVDIAFPCATONEIDEHDAELLIRKGC 420
DB 347 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCQVDIAFPCATONEIDEHDAELLIRKGC 406
QY 421 QYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVSGLEMTQNRMSLMTREVRD 480
DB 407 QYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVSGLEMTQNRMSLMTREVRD 466
QY 481 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKAGAV 526
DB 467 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKAGAV 512

RESULT 4
US-08-828-451-4
Sequence 4, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSES: Saliwanichik & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-451-4

Query Match 96.4%; Score 2621; DB 2; Length 512;
Best Local Similarity 97.3%; Pred. No. 1,1e-233;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTLVAKPIVAAPLAARPRCLAPWPCAWRSARVDRAKAVSLSEQISANDATTGDTA 60
DB 1 MOTLVAKPIVA-----CAWRSARVDRAKAVSLSEQISANDATTGDTA 46
QY 61 LQKAVKQMATKATGTEGLVHGINKPDPVROLTEIFMKDPEOEFMOAVREAVVSLQPVREK 120
DB 47 LQKAVKQMATKATGTEGLVHGINKPDPVROLTEIFMKDPEOEFMOAVREAVVSLQPVREK 106
QY 121 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 180
DB 107 RPBLPIFKQIVBERVITFRVSWLDDAGNLQVNRGFRVQSSAIGPYKGLRPHPSVNL 166
QY 181 SIMFLAFEOIFKNSLTLLPMGGGKGSDFPKGSDAEVWRFQSFMTTELQRIHSYQD 240
DB 167 SIMFLAFEOIFKNSLTLLPMGGGKGSDFPKGSDAEVWRFQSFMTTELQRIHSYQD 226
QY 241 VPADIGVAREIGYLFQYKRIKNTYGVLTLPKQEGSGEIRPEATGVALFVENVL 300
DB 227 VPADIGVAREIGYLFQYKRIKNTYGVLTLPKQEGSGEIRPEATGVALFVENVL 286
QY 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNNGFTREQLQAVQ 360
DB 287 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNNGFTREQLQAVQ 346
QY 361 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCQVDIAFPCATONEIDEHDAELLIRKGC 420
DB 347 DMKKKNSARISEKSDTAAYVVGDRRKWEIDCQVDIAFPCATONEIDEHDAELLIRKGC 406
QY 421 QYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVSGLEMTQNRMSLMTREVRD 480
DB 407 QYVEGANMPSSTNEAIHKYNKAGIYCPGKAANAGVAVSGLEMTQNRMSLMTREVRD 466
QY 481 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKAGAV 526
DB 467 KLERIMDIYDSAMGPRRRYVNDLAAGANIAGFTKVADAVAKAGAV 512

RESULT 5
US-08-541-033A-24
Sequence 24, Application US/08541033A
Patent No. 5879941


```
? GENERAL INFORMATION:
? APPLICANT: Schmidt, Robert R.
? TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
? TITLE OF INVENTION: RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
? TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
? NUMBER OF SEQUENCES: 26
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Saliwanchik & Saliwanchik
? STREET: 2421 N.W. 41st Street, Suite A-1
? CITY: Gainesville
? STATE: Florida
? COUNTRY: USA
? ZIP: 32606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/541,033A
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Whitlock, Ted W.
? REGISTRATION NUMBER: 36,965
? REFERENCE/DOCKET NUMBER: UP155
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (904) 375-8100
? TELEFAX: (904) 372-5800
? INFORMATION FOR SEQ ID NO: 24:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 487 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-541-033A-24

Query Match      92.2%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 2.8e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      521 KAQAV 526
      |||||
Db      482 KAQAV 487

RESULT 6
US-08-828-451-24
? Sequence 24, Application US/08828451
? Patent No. 5985634
? GENERAL INFORMATION:
? APPLICANT: Schmidt, Robert R.
? TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
? TITLE OF INVENTION: RELATING TO THE -- AND -SUBUNITS OF GLUTAMATE
? TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
? NUMBER OF SEQUENCES: 26
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Saliwanchik & Saliwanchik
? STREET: 2421 N.W. 41st Street, Suite A-1
? CITY: Gainesville
? STATE: Florida
? COUNTRY: USA
? ZIP: 32606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/828,451
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/541,033
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Whitlock, Ted W.
? REGISTRATION NUMBER: 36,965
? REFERENCE/DOCKET NUMBER: UP155
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (904) 375-8100
? TELEFAX: (904) 372-5800
? INFORMATION FOR SEQ ID NO: 24:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 487 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-828-451-24

Query Match      92.2%; Score 2508; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 2.8e-223;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 242 SEIRPEATGYGAVLVFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSD 301
Qy 341 SQGVYEPNGFTTRQLOAVQDMKKNSARISEYKSDTAVYVGRRKWEIQCVDIAFP 400
Db 302 SQGVYEPNGFTTRQLOAVQDMKKNSARISEYKSDTAVYVGRRKWEIQCVDIAFP 361
Qy 401 CATONEIDEHDAELLIKGCOYVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVS 460
Db 362 CATONEIDEHDAELLIKGCOYVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVS 421
Qy 461 GLENTORMSLMTREEVDRKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAV 520
Db 422 GLENTORMSLMTREEVDRKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAV 481
Qy 521 KAQGA 526
Db 482 KAQGA 487

RESULT 7

US-08-541-033A-26
Sequence 26, Application US/08541033A
Patent No. 5879941
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-541-033A-26

Query Match 90.6%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2,6e-219;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 MDATTGPTALQKAVKQMATKAGTEGLVHGKINPDVROLTEIMKXDPQOEFQAVREV 110
Db 1 MDATTGPTALQKAVKQMATKAGTEGLVHGKINPDVROLTEIMKXDPQOEFQAVREV 60
Qy 111 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDAGNLQVNRGRFVQYSSAIGPYK 170
Db 61 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDAGNLQVNRGRFVQYSSAIGPYK 120

Qy 171 GLRHPSEVNLIMKFLAFEOIFKNSLTTLLPMGGKGSDDPKGSDAEVNRFCOSFMT 230
Db 121 GLRHPSEVNLIMKFLAFEOIFKNSLTTLLPMGGKGSDDPKGSDAEVNRFCOSFMT 180
Qy 231 LORHISYVDVPAAGDIGVAREIGYLFQYKRTITKNTGVLTJPKQOYGSSEIRPEATGY 290
Db 181 LORHISYVDVPAAGDIGVAREIGYLFQYKRTITKNTGVLTJPKQOYGSSEIRPEATGY 240
Qy 291 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGVYEPNG 350
Db 241 GAVLFVENVLKDKGESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLSLSDSQGVYEPNG 300
Qy 351 FTREQLQAVQDMKKNSARISEYKSDTAVYVGRRKWEIQCVDIAFPQATONEIDEH 410
Db 301 FTREQLQAVQDMKKNSARISEYKSDTAVYVGRRKWEIQCVDIAFPQATONEIDEH 360
Qy 411 DAEILLIKGCOYVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVSGLONTORMS 470
Db 361 DAEILLIKGCOYVEGAMNPSTNEAIHKYNKAGIYCPGKAANGVAVSGLONTORMS 420
Qy 471 LMTREEVDRKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGA 526
Db 421 LMTREEVDRKLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAQGA 476

RESULT 8

US-08-828-451-26
Sequence 26, Application US/08828451
Patent No. 5985634
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-451-26

Query Match 90.6%; Score 2465; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2,6e-219;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 MDATTGDTALQKAKOMATKAGTEGLVHGINKNDVRLTTEIFMKDPEQOEPMQAVREV 110
DB 1 MDATTGDTALQKAKOMATKAGTEGLVHGINKNDVRLTTEIFMKDPEQOEPMQAVREV 60
QY 111 AVSLOPVEKREPELLPIFKQIVPEPRVITTFVSVLDDAGNLQVNRGRVOYSSAIGPYKG 170
DB 61 AVSLOPVEKREPELLPIFKQIVPEPRVITTFVSVLDDAGNLQVNRGRVOYSSAIGPYKG 120
QY 171 GLRHPSPNLSIMELFLPEQIFKNSLTLPMPGSGKGSDFDPKSKDAEVRFCQSPMTE 230
DB 121 GLRHPSPNLSIMELFLPEQIFKNSLTLPMPGSGKGSDFDPKSKDAEVRFCQSPMTE 180
QY 231 LQHRISYVODVPADIGVAREIGYLFQYKRIKNTGVLTLPKQOYSGSEIRPEATGY 290
DB 181 LQHRISYVODVPADIGVAREIGYLFQYKRIKNTGVLTLPKQOYSGSEIRPEATGY 240
QY 291 GAVLFVENVLKDKESLKGKRCVSGAGNVAQYCAELLLEKGAIVLSLSDQGYVPEPN 350
DB 241 GAVLFVENVLKDKESLKGKRCVSGAGNVAQYCAELLLEKGAIVLSLSDQGYVPEPN 300
QY 351 FTREQLAVODMKKQNSARISEKSDTAAYVGDPRKPMELDCQVDIAFPATONEIDEH 410
DB 301 FTREQLAVODMKKQNSARISEKSDTAAYVGDPRKPMELDCQVDIAFPATONEIDEH 360
QY 411 DAEILLIKHCQYVVEGANMPESTNEAIHKYNKAGIITPCGKANAAGVAVSGLEMTQNRMS 470
DB 361 DAEILLIKHCQYVVEGANMPESTNEAIHKYNKAGIITPCGKANAAGVAVSGLEMTQNRMS 420
QY 471 LNMTRREVRDKLEIMKDIYDSANGSPSRNVDLAAGNIAGTFTKADAVAKOAV 526
DB 421 LNMTRREVRDKLEIMKDIYDSANGSPSRNVDLAAGNIAGTFTKADAVAKOAV 476

RESULT 9

US-09-252-991A-20646
; Sequence 20646, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20646
; LENGTH: 450
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20646

Query Match 48.1%; Score 1309; DB 4; Length 450;
Best Local Similarity 59.2%; Pred. No. 2.2e-112;

Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;

QY 86 VRQLLTFEIMKDPQOEPMQAVREVAVSLQVFEKREPELL-IFKQIVPEPRVITTFVS 143
DB 10 VDALEFLKRRDPQPEFHQAVEEVLRLSLMPFLANPHYLEAGIIRIIVEPERALIFRPV 69
QY 144 WLDDAGNLQVNRGRVOYSSAIGPYKGLRHPSPNLSIMKFLAFOQIFKNSLTLPMPG 203
DB 70 WVDQGVAVNRGRVOYSSAIGPYKGLRHPSPNLSIMKFLAFOQIFKNSLTLPMPG 129
QY 204 GKGSGDDPKGSKDAEVRFCQSPMTELQRIISYVODVPADIGVAREIGYLFQYKRI 263
DB 130 GKGSGDDPKGSKDAEVRFCQSPMTELQRIISYVODVPADIGVAREIGYLFQYKRI 189
QY 264 TKNTYGVLTLPKQOYSGSEIRPEATGYGAVLFVENVLKDKESLKGKRCVSGAGNVAQY 323

DB 190 SNOFTSVLTGKGSYSGSLRPEATFGCYFAQEMLKRGRCFDOQRAVSISSGNVAQY 249
QY 324 CAELLEKGAIVLSLSDQGYVPEPNFTREQLAVODMKKQNSARISEKSDTAAYV 363
DB 250 AAKRVEMGKGVLSLSDQGYVPEPNFTREQLAVODMKKQNSARISEKSDTAAYV 308
QY 384 DRRKPMELDCQVDIAFPATONEIDEHDAELLIKHCQYVVEGANMPESTNEAIHKYNKAG 443
DB 309 EGRPMGLAC--DIALPCATQNELDAEDARRLLANGCVCAEGANMPESTLEAVDLFLEAG 366
QY 444 IITPCGKANAAGVAVSGLEMTQNRMSLMTREVRDKLEIMKDIYDSA-MPSRRVNY 502
DB 367 ILVAPGASVAGVAVSGLEMTQNRMSLMTREVRDKLEIMKDIYDSA-MPSRRVNY 426
QY 503 DLAAGNIAGTFTKADAVAKOAV 526
DB 427 NYKGANIAGFVAVKADAMLAQGV 450

RESULT 10

US-09-328-352-5725
; Sequence 5725, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5725
; LENGTH: 467
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5725

Query Match 46.2%; Score 1257.5; DB 4; Length 467;
Best Local Similarity 55.9%; Pred. No. 1.4e-107;

Matches 256; Conservative 61; Mismatches 128; Indels 13; Gaps 5;

QY 77 LVH-----GINKPDRQLTTEIFMKDPEQOEPMQAVREVAVSLQVFEKREPELL-IF 128
DB 11 LIHYAEDRALKKNINNEFLINVAQARDPQPEFLQAVEEWMTLMPFIEKNEPRYABQGL 70
QY 129 KOIVPEPRVITTFVSVLDDAGNLQVNRGRVOYSSAIGPYKGLRHPSPNLSIMKFLA 188
DB 71 ERIVEPRVITTFVSVLDDAGNLQVNRGRVOYSSAIGPYKGLRHPSPNLSIMKFLA 130
QY 189 EQIFKNSLTLPMPGSGKGSDFDPKSKDAEVRFCQSPMTELQRIISYVODVPADIGV 248
DB 131 EQIFKNSLTLPMPGSGKGSDFDPKSKDAEVRFCQSPMTELQRIISYVODVPADIGV 190
QY 249 GAREIGYLFQYKRIKNTGVLTLPKQOYSGSEIRPEATGYAVLFVENVLKDKESL 308
DB 191 GAREIGYLFQYKRIKNTGVLTLPKQOYSGSEIRPEATGYAVLFVENVLKDKESL 250
QY 309 GRCVSGAGNVAQYCAELLLEKGAIVLSLSDQGYVPEPNFTREQLAVODMKKQNS 368
DB 251 GKTVISISGSGNVAQYAEKAMFLGAKRVTLSDNGTVYLLKNGFTDLAEVMELEKRIK 309
QY 369 ARISEKSDTAAYVGDPRKPMELDCQVDIAFPATONEIDEHDAELLIKHCQYVVEGAN 428
DB 310 GRISERPAKSGFVEKPTPMH--EVDIALPCATQNELGDAKTLIANGVCAEGAN 367
QY 429 MPSTNEAIHKYNKAGIITPCGKANAAGVAVSGLEMTQNRMSLMTREVRDKLEIMK 468
DB 368 MPSTLEAVEHFIAKILVAPGASVAGVAVSGLEMTQNRMSLMTREVRDKLEIMK 427
QY 489 IYDSAM--GPSRRVNYDLAAGNIAGTFTKADAVAKOAV 524
DB 428 IHANCVRYGTEDGTAVYVDGANIAGFVAVKADAMLAQGV 465

RESULT 11

US-09-134-000C-3884

Sequence 3884, Application US/09134000C
Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3884

LENGTH: 448

TYPE: PR

ORGANISM: Enterococcus faecalis

US-09-134-000C-3884

Query Match 45.4%; Score 1234.5; DB 4; Length 448;
Best Local Similarity 55.9%; Pred. No. 1.7e-105;
Matches 250; Conservative 63; Mismatches 123; Indels 11; Gaps 6;

QY 86 VRLLTEIFMKDPQOEPMQAVREAVASLOPVEKRELLP--IFKQIYBERVITRRVS 143

DB 7 VKNIOEKIHQDQCTEYLQAVDEFLPYVEGFLEKNPQYIEANVGLVIFPERIFQFRVP 66

QY 144 WLDAGNLQVNRGRVQYSSAIGPYKGLRPHPSVNLISIMKFLAEQIFKNSLTLLPMG 203

DB 67 WODQGMHVRGKRVQYNSAIGPYKGLRPHPSVNLISIMKFLAEQIFKNSLTLLPMG 126

QY 204 GKGSDPDPKGSPPAEVRFQSFMTLORHISYVQDPADIGVAREIGYLFQYKRI 263

DB 127 GKGSDPDPKGSPPAEVRFQSFMTLORHISYVQDPADIGVAREIGYLFQYKRI 186

QY 264 TKNYTVLTPKQEGYSEIRPEATGYAVLFVENVLKDGESLKGKRCIVSGANVAQY 323

DB 187 RNYDAGVLTGKPLGFGSLRPEATGYAVLFVENVLKDGESLKGKRCIVSGANVAQY 246

QY 324 CAELLKGAIVLSLSQGYVEPNFTREQLQAVQDMKKNSARISEKST--AVY 381

DB 247 AMERATLGAIVTICSDSSGVEYDPEGI--DVALVVELKEKNEB-RISKVETTRKQATY 302

QY 382 VGDRRKPEMLDQVDIAFPACATONEIDEHDAELIKHGCQYVVGANMPSTNEAIIHKYK 441

DB 303 Y-DKESVWNEFTAYDIALPCATONEINEKQAAIIVKGVAVAGANMPCTLEAVAVPAK 361

QY 442 AGIITCPKKAAGVAVSGLEMTQNRMSLWTRREVRDKLERIMKDIYDSAMPSRRYV 501

DB 362 SAVIYCPKKAAGVAVSALEMSQNRRLAMSEKVDQMLDMQNIYERCRDTANEYQ 421

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

QY 502 V--DLAAGANIAGTQVADAVAKAGAV 526

DB 422 ARDNFVLGANIAGTQVADAVAKAGAV 448

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4489

LENGTH: 448

TYPE: PR

ORGANISM: Streptococcus pneumoniae

US-09-583-110-4489

Query Match 44.9%; Score 1221; DB 4; Length 448;
Best Local Similarity 55.7%; Pred. No. 3.1e-104;
Matches 248; Conservative 64; Mismatches 125; Indels 8; Gaps 4;

QY 86 VRLLTEIFMKDPQOEPMQAVREAVASLOPVEKRELLP--IFKQIYBERVITRRVS 143

DB 8 IQSVFTVKARNGHEAEFLQAVEEFPMTLPVEKHEVEYIEENILARITEPERVVSFRVP 67

QY 144 WLDAGNLQVNRGRVQYSSAIGPYKGLRPHPSVNLISIMKFLAEQIFKNSLTLLPMG 203

DB 68 WVDKDKI QVNRGRVQYSSAIGPYKGLRPHPSVNLISIMKFLAEQIFKNSLTLLPMG 127

QY 204 GKGSDPDPKGSPPAEVRFQSFMTLORHISYVQDPADIGVAREIGYLFQYKRI 263

DB 128 GKGSDPDPKGSPPAEVRFQSFMTLORHISYVQDPADIGVAREIGYLFQYKRI 187

QY 264 TKNYTVLTPKQEGYSEIRPEATGYAVLFVENVLKDGESLKGKRCIVSGANVAQY 323

DB 188 NQFAGVLTGKPLGFGSLRPEATGYAVLFVENVLKDGESLKGKRCIVSGANVAQY 247

QY 324 CAELLKGAIVLSLSQGYVEPNFTREQLQAVQDMKKNSARISEKST--AVY 383

DB 248 ALQATLGAIVTICSDSSGVEYDPEGI--DVALVVELKEKNEB-RISKVETTRKQATY 303

QY 384 DRKPEMLDQVDIAFPACATONEIDEHDAELIKHGCQYVVGANMPSTNEAIIHKYK 443

DB 304 HEGTVMYAGNYDIALPCATONEINEKQAAIIVKGVAVAGANMPCTLEAVAVPAK 363

QY 444 IYCPKKAAGVAVSGLEMTQNRMSLWTRREVRDKLERIMKDIYDSAMPSRRYV 502

DB 364 ILVGPAAAGVAVSALEMSQNRRLAMSEKVDQMLDMQNIYERCRDTANEYQ 423

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

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DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

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QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

DB 424 KQYLAGANIAAFENVANAMIAQIV 448

QY 503 -DLAAGANIAGTQVADAVAKAGAV 526

FILING DATE: 01-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,058
FILING DATE: 02-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kokulie, Paul K.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 81163/241766
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-861-3503
TELEFAX: (202)-822-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-886-640-3

Query Match 44.2%; Score 1201; DB 2; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.2e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 86 VRQLTEIFMKDPEQEFMVAAREVAVSLQPEKRPET--LPFKQIYEPERVITFRVS 143
DB 7 LESFLNHVQKRDPNQTEFAQAVREAVMTTLMPLEQNPVKRQMSLRLRVEREVIQFRVY 66
QY 144 WLDNAGLQVNRGRVQYSSAIGPYKGLRFRHSVNLSTMKFLAFQIFKNSLTLLPMG 203
DB 67 WVDNRNOIQNRRMRVQFSSAIGPYKGMFRHPSVNLSTIKFLGFQTFKNAITLLPMG 126
QY 204 GKGSDDPDKPKSGDAEVRFCQSFMTLORHISYVODVPAGDIGVAREIGYLFQYKRI 263
DB 127 GKGSDDPDKPKSGEVRFCQALMTLRYHLGADTDVPAGDIGVGREYFPMAGMKKL 186
QY 264 TKNYTGVLTPKQGEYSGSEIRPEATGYAVLFVENVLKDKGESLKGKRLVSGAGNVAQY 323
DB 187 SNNYACVFTGKGLSFGSLIRPEATGYGLVYFTEAMLKRGHMGFEGRVSVSSGNAQY 246
QY 324 CAELLLEKGAIVLSDSQGYVYEPNGFTREQLQAVODMKKNSARISYKSDTAVYVG 383
DB 247 AIEKMEFGARVITVASSSGTVVDESGETYKELARLIEI-KASRDGVADYAKEFGVLYL 305
QY 384 DRKPMELDCQVDAIPCATONEIDEHDAELIKHGQYVVEGAMPSTNEAIHKYNKAG 443
DB 306 EGQPMSL--PVDIALPCATONELVDVAHQLIANGVAVABGANMPTTEATELFOQAG 363
QY 444 IIVCPKAAAGVAVASGLEMTONRMSLNTREBVRDKLERIMKDIYDSAM--GPSRRY 500
DB 364 VLFAPGAAAGVAVASGLEMAQNAARLGWAKAKVDAARLHIMLDIHACVHDGGEQET 423
QY 501 NVDLAAGANTAGFTKADAVAKAGAV 526
DB 424 N--YVQGANIAGFVKVADAMLAQGI 447

RESULT 14
US-08-884-235-11
Sequence 11, Application US/08884235
Patent No. 6329573
GENERAL INFORMATION:
APPLICANT: Lightfoot, David A.
APPLICANT: Long, Lynn M.
APPLICANT: Lightfoot, Maria E. Vidal
TITLE OF INVENTION: PLANTS CONTAINING THE gdhA GENE AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,235
FILING DATE: 27-JUN-1997
CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 residues
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-884-235-11

Query Match 44.2%; Score 1201; DB 3; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.2e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 86 VRQLTEIFMKDPEQEFMVAAREVAVSLQPEKRPET--LPFKQIYEPERVITFRVS 143
DB 7 LESFLNHVQKRDPNQTEFAQAVREAVMTTLMPLEQNPVKRQMSLRLRVEREVIQFRVY 66
QY 144 WLDNAGLQVNRGRVQYSSAIGPYKGLRFRHSVNLSTMKFLAFQIFKNSLTLLPMG 203
DB 67 WVDNRNOIQNRRMRVQFSSAIGPYKGMFRHPSVNLSTIKFLGFQTFKNAITLLPMG 126
QY 204 GKGSDDPDKPKSGDAEVRFCQSFMTLORHISYVODVPAGDIGVAREIGYLFQYKRI 263
DB 127 GKGSDDPDKPKSGEVRFCQALMTLRYHLGADTDVPAGDIGVGREYFPMAGMKKL 186
QY 264 TKNYTGVLTPKQGEYSGSEIRPEATGYAVLFVENVLKDKGESLKGKRLVSGAGNVAQY 323
DB 187 SNNYACVFTGKGLSFGSLIRPEATGYGLVYFTEAMLKRGHMGFEGRVSVSSGNAQY 246
QY 324 CAELLLEKGAIVLSDSQGYVYEPNGFTREQLQAVODMKKNSARISYKSDTAVYVG 383
DB 247 AIEKMEFGARVITVASSSGTVVDESGETYKELARLIEI-KASRDGVADYAKEFGVLYL 305
QY 384 DRKPMELDCQVDAIPCATONEIDEHDAELIKHGQYVVEGAMPSTNEAIHKYNKAG 443
DB 306 EGQPMSL--PVDIALPCATONELVDVAHQLIANGVAVABGANMPTTEATELFOQAG 363
QY 444 IIVCPKAAAGVAVASGLEMTONRMSLNTREBVRDKLERIMKDIYDSAM--GPSRRY 500
DB 364 VLFAPGAAAGVAVASGLEMAQNAARLGWAKAKVDAARLHIMLDIHACVHDGGEQET 423
QY 501 NVDLAAGANTAGFTKADAVAKAGAV 526
DB 424 N--YVQGANIAGFVKVADAMLAQGI 447

RESULT 15
US-08-370-193A-11
Sequence 11, Application US/08370193A
Patent No. 5573945
GENERAL INFORMATION:
APPLICANT: ONO, Eiji
APPLICANT: TSUTIMOTO, NOBUHARU
APPLICANT: MATSUI, KAZUHIKO
APPLICANT: KURAHASHI, KAZUHIKO
TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING
L-GLUTAMIC ACID BY FERMENTATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,193A
FILING DATE: 09-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-714-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-370-193A-11

Query Match 44.1%; Score 1200; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 2.7e-102;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

QY 86 VRQLLTFELFMKDPQOEFMQAVREVAVSLQPFKEKPEL--LPFKQIVPEPERVITFRVS 143
DB 7 LESFLNHQKRDPNTEBPAQVREVMWTLWPFLEQNPFRQMSLERLVERPERVIOFRVV 66
QY 144 WLDNAGNLQVNRGRFRVQSSAIGPYKGLRPHPSVNLSTMKFLAEOIFKNSLTLLPMGG 203
DB 67 WVDNRNOIQVNRARVOPSSAIGPYKGMRPHSPVNLSTLFLGFEQTFKNAITLLPMGG 126
QY 204 GKGSDFDPKGSQDAEVRFCOSFWTELQRIHSYVQDVPAQDVGVAEIGYLPFGYKRI 263
DB 127 GKGSDFDPKGSQDAEVRFCQALMTLRYHLGADTVPAQDVGVAEIGYLPFGYKRI 186
QY 264 TKNYTGVLTPEKQYSGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGAGNVAQY 323
DB 187 SNNYACVFTGKGLSPGSLIRPEATGYGAVLFTEAMLKRHGMPEGRVSVSSGNAQY 246
QY 324 CAELLEKGAIVLSDSQGYVYEPNCFTRQLOAVODMKKNSARISEYKSDTAVVYG 383
DB 247 AIEKAMEFGARVITYASDSSTGVVDESGFTKEKLRLIEI-KASRDGRVADYAKEFGLVYL 305
QY 384 DRKPEWELDCQVDIAFPATONEIDEHDAELLIKGCQYVVEGAMMPSTNEAIHKYKAG 443
DB 306 EGQQPMSEL--PVDIALPCATONELDVAHQILANGVAVAEGAMMPPTTEATELFOQAG 363
QY 444 IIVPGKAANAGVAVSGLEMTQNRMSLMTREVRDLERIMKOIYDSAM--GPSRY 500
DB 364 VLPFAFGKDAANAGVAVSGLEMTQNRMSLMTREVRDLERIMKOIYDSAM--GPSRY 423
QY 501 NVDLAAGANTAGFTKVADAVKAGAV 526
DB 424 N--YVQGANIAGFVKVADAMLAQGI 447

Search completed: July 9, 2005, 18:36:41
Job time : 45 secs

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OM protein - protein search, using sw model1

Run on: July 9, 2005, 18:29:13 ; Search time 166 Seconds

(without alignments)
1224.155 Million cell updates/sec

Title: US-10-627-886-2

Perfect score: 2720
Sequence: 1 MGNALVAKPVAAPLAAPR.....GANIAGFTXADAVKAGAV 526

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 1726216 seqs, 38630316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubppaa/US10G_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubppaa/US10H_PUBCOMB.pep.*
- 21: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2720	100.0	526	9 US-09-070-844-2	Sequence 2, Appl1
2	2720	100.0	526	16 US-10-627-886-2	Sequence 2, Appl1
3	2621	96.4	512	9 US-09-070-844-4	Sequence 4, Appl1
4	2621	96.4	512	16 US-10-627-886-4	Sequence 4, Appl1
5	2508	92.2	487	9 US-09-070-844-24	Sequence 24, Appl1
6	2508	92.2	487	16 US-10-627-886-24	Sequence 24, Appl1
7	2465	90.6	476	9 US-09-070-844-26	Sequence 26, Appl1
8	2465	90.6	476	16 US-10-627-886-26	Sequence 26, Appl1
9	1309	48.1	445	15 US-10-282-122A-66687	Sequence 66687, A
10	1297.5	47.7	444	15 US-10-282-122A-65129	Sequence 65129, A
11	1294.5	47.6	444	15 US-10-282-122A-66041	Sequence 66041, A

12	1294.5	47.6	444	15	US-10-275-026A-152	Sequence 152, App
13	1287.5	47.3	449	15	US-10-282-122A-67538	Sequence 67538, A
14	1281	47.1	445	15	US-10-369-493-13947	Sequence 13947, A
15	1259	46.3	454	15	US-10-369-493-9839	Sequence 9839, App
16	1257.5	46.2	462	15	US-10-282-122A-45200	Sequence 45200, A
17	1239.5	45.6	448	15	US-10-282-122A-57310	Sequence 57310, A
18	1238	45.5	449	14	US-10-260-877-90	Sequence 90, Appl1
19	1238	45.5	449	15	US-10-282-122A-58096	Sequence 58096, A
20	1230.5	45.2	449	15	US-10-282-122A-72329	Sequence 72329, A
21	1230	45.2	449	15	US-10-282-122A-66870	Sequence 66870, A
22	1214	44.6	448	15	US-10-282-122A-74024	Sequence 74024, A
23	1212	44.6	448	17	US-10-472-928-2632	Sequence 2632, App
24	1210.5	44.5	458	15	US-10-369-493-17284	Sequence 17284, A
25	1207.5	44.4	464	15	US-10-282-122A-51278	Sequence 51278, A
26	1205.5	44.3	444	15	US-10-369-493-617	Sequence 617, App
27	1205.5	44.3	444	15	US-10-282-122A-48442	Sequence 48442, A
28	1201	44.2	447	15	US-10-369-493-859	Sequence 859, App
29	1199	44.2	447	15	US-10-282-122A-43284	Sequence 43284, A
30	1199	44.1	443	15	US-10-282-122A-52117	Sequence 52117, A
31	1196.5	44.0	466	15	US-10-425-114-72861	Sequence 72861, A
32	1195.5	44.0	468	15	US-10-369-493-8215	Sequence 8215, App
33	1194	43.9	438	15	US-10-369-493-10621	Sequence 10621, A
34	1194	43.8	447	15	US-10-282-122A-60243	Sequence 60243, A
35	1185	43.6	447	9	US-09-738-626-6982	Sequence 6982, App
36	1182.5	43.5	448	15	US-10-282-122A-53998	Sequence 53998, A
37	1181	43.4	447	15	US-10-282-122A-75593	Sequence 75593, A
38	1180.5	43.4	458	15	US-10-282-122A-60810	Sequence 60810, A
39	1180	43.4	447	15	US-10-369-493-295	Sequence 295, App
40	1178	43.3	447	15	US-10-282-122A-72769	Sequence 72769, A
41	1177.5	43.3	446	15	US-10-282-122A-68627	Sequence 68627, A
42	1169.5	43.0	446	15	US-10-282-122A-62874	Sequence 62874, A
43	1169	43.0	442	15	US-10-282-122A-55644	Sequence 55644, A
44	1153	42.4	447	15	US-10-282-122A-78288	Sequence 78288, A
45	1150	42.3	448	15	US-10-282-122A-58700	Sequence 58700, A

ALIGNMENTS

RESULT 1
US-09-070-844-2
Sequence 2, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanhik & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UFI55

TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-2

Query Match 100.0%; Score 2720; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 5.7e-236;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTLVAKPIVAAPLAAPRCCLAPWPCAMWSAKRDVRAKAVSLAEQISAMDATTGDTA 60
DB 1 MOTLVAKPIVAAPLAAPRCCLAPWPCAMWSAKRDVRAKAVSLAEQISAMDATTGDTA 60
QY 61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQEFMOAVREAVASLQVFEK 120
DB 61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQEFMOAVREAVASLQVFEK 120
QY 121 RPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
DB 121 RPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
QY 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKKSDAEVRFCQSFTELQRHISYVD 240
DB 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKKSDAEVRFCQSFTELQRHISYVD 240
QY 241 VPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKGOEYGSSEIRPATGYAVLFVENVL 300
DB 241 VPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKGOEYGSSEIRPATGYAVLFVENVL 300
QY 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTREQLQAVQ 360
DB 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTREQLQAVQ 360
QY 361 DMKKKNSARISEYKSDTAAYVGDRRKPEWLDQVDAFPACATONEIDEHDAELLKHGC 420
DB 361 DMKKKNSARISEYKSDTAAYVGDRRKPEWLDQVDAFPACATONEIDEHDAELLKHGC 420
QY 421 QYVEGANMPSTNEAIHKYNKAGIICPGKAAAGVAVSGLEMTQNRMSLNTREVRD 480
DB 421 QYVEGANMPSTNEAIHKYNKAGIICPGKAAAGVAVSGLEMTQNRMSLNTREVRD 480
QY 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526
DB 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526

RESULT 2

US-10-627-886-2
Sequence 2, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

ATTORNEY: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606-6669

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95

ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-627-886-2

Query Match 100.0%; Score 2720; DB 16; Length 526;
Best Local Similarity 100.0%; Pred. No. 5.7e-236;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTLVAKPIVAAPLAAPRCCLAPWPCAMWSAKRDVRAKAVSLAEQISAMDATTGDTA 60
DB 1 MOTLVAKPIVAAPLAAPRCCLAPWPCAMWSAKRDVRAKAVSLAEQISAMDATTGDTA 60
QY 61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQEFMOAVREAVASLQVFEK 120
DB 61 LQKAVKQMATKATGEGVHGIKNPDVROLTEIFMKDPEQEFMOAVREAVASLQVFEK 120
QY 121 RPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
DB 121 RPELLPIFKQIVPERVITFRVSWLDAGNLQVNRGFRVQSSAIGYKGLRPHSVNL 180
QY 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKKSDAEVRFCQSFTELQRHISYVD 240
DB 181 SIMFLAFEOIFKNSLTLLPMGGKGSDFDPKKSDAEVRFCQSFTELQRHISYVD 240
QY 241 VPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKGOEYGSSEIRPATGYAVLFVENVL 300
DB 241 VPAGDIGVAREIGYLFQGYKRITKNYTGVLTPKGOEYGSSEIRPATGYAVLFVENVL 300
QY 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTREQLQAVQ 360
DB 301 KDKGESLKGRKCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVEPNGFTREQLQAVQ 360
QY 361 DMKKKNSARISEYKSDTAAYVGDRRKPEWLDQVDAFPACATONEIDEHDAELLKHGC 420
DB 361 DMKKKNSARISEYKSDTAAYVGDRRKPEWLDQVDAFPACATONEIDEHDAELLKHGC 420
QY 421 QYVEGANMPSTNEAIHKYNKAGIICPGKAAAGVAVSGLEMTQNRMSLNTREVRD 480
DB 421 QYVEGANMPSTNEAIHKYNKAGIICPGKAAAGVAVSGLEMTQNRMSLNTREVRD 480
QY 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526
DB 481 KLERIMKDIYDSAMGPSRRYVNDLAAGANIAGFTKVADAVKAGAV 526

RESULT 3

US-09-070-844-4
Sequence 4, Application US/09070844

Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-4

Query Match 96.4%; Score 2621; DB 9; Length 512;
Best Local Similarity 97.3%; Pred. No. 4.6e-227;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVAAPLAARPCLAAPWPCAWRSARADVRAKAVSLSEBOISAMDATGDTA 60
DB 1 MOTALVAKPIVA-----CAWRSARADVRAKAVSLSEBOISAMDATGDTA 46
QY 61 LQKAVKQMATKAGTGLVHGIKNPDVROLTEIFMKDPEOQEFMQAVREVAVSLQPVFEK 120
DB 47 LQKAVKQMATKAGTGLVHGIKNPDVROLTEIFMKDPEOQEFMQAVREVAVSLQPVFEK 106
QY 121 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGRVQYSSAIGYKGLAFHPSVNL 180
DB 107 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGRVQYSSAIGYKGLAFHPSVNL 166
QY 181 SIMKFLAFEOIFKNSLTLTPMGSGKSGSDPDKGSDAEVRFCOSFMTTELQRIHSYQD 240
DB 167 SIMKFLAFEOIFKNSLTLTPMGSGKSGSDPDKGSDAEVRFCOSFMTTELQRIHSYQD 226
QY 241 VPADIGVAREIGYLFQYRITKNTYGVLTTPKQEGYSGSEIRPEATGYAVLFEVNL 300
DB 227 VPADIGVAREIGYLFQYRITKNTYGVLTTPKQEGYSGSEIRPEATGYAVLFEVNL 286
QY 301 KDKGESLKGRCCLVSGAGNVAOYCAEILLEKGAIVLSLSDSGYVYBNGFTREQLQAVQ 360
DB 287 KDKGESLKGRCCLVSGAGNVAOYCAEILLEKGAIVLSLSDSGYVYBNGFTREQLQAVQ 346
QY 361 DMKKKNSARISEYKSDTAVVVGDRRKPEWELDCQVDIAFPCATONEIDEHDAELLIKGC 420
DB 347 DMKKKNSARISEYKSDTAVVVGDRRKPEWELDCQVDIAFPCATONEIDEHDAELLIKGC 406

QY 421 QYVEGANMPESTNEAIHKYKAGIIYCRKAANGVAVSGLSEMTONRMSLMTREEVRD 480
DB 407 QYVEGANMPESTNEAIHKYKAGIIYCRKAANGVAVSGLSEMTONRMSLMTREEVRD 466
QY 481 KLERIMDIYDSAMPSPRRYVNDLAAGANLAGFTKVADAVAKQAV 526
DB 467 KLERIMDIYDSAMPSPRRYVNDLAAGANLAGFTKVADAVAKQAV 512

RESULT 4
US-10-627-886-4
Sequence 4, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-627-886-4

Query Match 96.4%; Score 2621; DB 16; Length 512;
Best Local Similarity 97.3%; Pred. No. 4.6e-227;
Matches 512; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MOTALVAKPIVAAPLAARPCLAAPWPCAWRSARADVRAKAVSLSEBOISAMDATGDTA 60
DB 1 MOTALVAKPIVA-----CAWRSARADVRAKAVSLSEBOISAMDATGDTA 46
QY 61 LQKAVKQMATKAGTGLVHGIKNPDVROLTEIFMKDPEOQEFMQAVREVAVSLQPVFEK 120
DB 47 LQKAVKQMATKAGTGLVHGIKNPDVROLTEIFMKDPEOQEFMQAVREVAVSLQPVFEK 106
QY 121 RPELLPIFKQIVBERVITFRVSWLMDAGNLQVNRGRVQYSSAIGYKGLAFHPSVNL 180

Db 107 RPELPIFKQIVBERVITFRVSMLDAGNLQVNRGEFVQSSAIGPYKGLRHPSPVNL 166
Qy 181 SIMFLAFEOIFKNSLITLPMGGGKGSDFDPKGSDAEVRFPQSFMTLORHISYVOD 240
Db 167 SIMFLAFEOIFKNSLITLPMGGGKGSDFDPKGSDAEVRFPQSFMTLORHISYVOD 226
Qy 241 VPADIGGAREIGLFGQYRITKNYTVLTLPKGOEYXGSEIRPEATYGAUVFVENVL 300
Db 227 VPADIGGAREIGLFGQYRITKNYTVLTLPKGOEYXGSEIRPEATYGAUVFVENVL 286
Qy 301 KDKESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLISDSQGYVEPNFTREQLQAVQ 360
Db 287 KDKESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLISDSQGYVEPNFTREQLQAVQ 346
Qy 361 DMKKKNSARISEKSDTAVVGVDRRKPMELDCQVDIAFPQATQNEIDEHDAELLIRHC 420
Db 347 DMKKKNSARISEKSDTAVVGVDRRKPMELDCQVDIAFPQATQNEIDEHDAELLIRHC 406
Qy 421 QYVEGANMPSTNEAIHKYNKAGIITCPGKAANAGVAVSGLENTQNRMSLNTREEVVD 480
Db 407 QYVEGANMPSTNEAIHKYNKAGIITCPGKAANAGVAVSGLENTQNRMSLNTREEVVD 466
Qy 481 KLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAVTAQGA 526
Db 467 KLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAVTAQGA 512

RESULT 5

US-09-070-844-24
Sequence 24, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-070-844-24

Query Match 92.2%; Score 2508; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 6,6e-217;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AVSLSEQISAMDATGDTFTLQKAVKQMATKAGTEGVHGIKNPDVROLITLIFMDPEQ 100
Db 2 AVSLSEQISAMDATGDTFTLQKAVKQMATKAGTEGVHGIKNPDVROLITLIFMDPEQ 61
Qy 101 QEFMQAVREAVASLOPFEERPELPIFKQIVBERVITFRVSMLDAGNLQVNRGEFVQ 160
Db 62 QEFMQAVREAVASLOPFEERPELPIFKQIVBERVITFRVSMLDAGNLQVNRGEFVQ 121
Qy 161 YSSAIGPYKGLRHPSPVNLISIMKFLAFEOIFKNSLITLPMGGGKGSDFDPKGSDAEV 220
Db 122 YSSAIGPYKGLRHPSPVNLISIMKFLAFEOIFKNSLITLPMGGGKGSDFDPKGSDAEV 181
Qy 221 MRFQSFMTLORHISYVODVPAGDIGVAREIGYFGQYKRTKNYTVLTLPKGOEYXG 280
Db 182 MRFQSFMTLORHISYVODVPAGDIGVAREIGYFGQYKRTKNYTVLTLPKGOEYXG 241
Qy 281 SEIRPEATYGAUVFVENVLKDKESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLISLD 340
Db 242 SEIRPEATYGAUVFVENVLKDKESLKGKRCCLVSGAGNVAQYCAELLEKGAIVLISLD 301
Qy 341 SOGYVEPNFTREQLQAVQDMKKKNSARISEKSDTAVVGVDRRKPMELDCQVDIAFP 400
Db 302 SOGYVEPNFTREQLQAVQDMKKKNSARISEKSDTAVVGVDRRKPMELDCQVDIAFP 361
Qy 401 CATQNEIDEHDAELLIRHGCQYVEGANMPSTNEAIHKYNKAGIITCPGKAANAGVAVS 460
Db 362 CATQNEIDEHDAELLIRHGCQYVEGANMPSTNEAIHKYNKAGIITCPGKAANAGVAVS 421
Qy 461 GLENTQNRMSLNTREEVVDKLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAV 520
Db 422 GLENTQNRMSLNTREEVVDKLERIMKDIYDSAMGSPSRVNVDLAAGANIAGFTKVADAV 481
Qy 521 KAQGA 526
Db 482 KAQGA 487

RESULT 6

US-10-627-886-24
Sequence 24, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE '-' AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: LLOYD, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-627-886-24

Query Match 92.2%; Score 2508; DB 16; Length 487;
Best Local Similarity 100.0%; Pred. No. 6,6e-217;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AVSLSEIOISAMDATGDTALQKAVKQMATAGTEGLVHGINKPDVROLTLTEIFMKDEQ 100
DB 2 AVSLSEIOISAMDATGDTALQKAVKQMATAGTEGLVHGINKPDVROLTLTEIFMKDEQ 61

QY 101 QEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGRVQ 160
DB 62 QEFMOAVREVAVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGRVQ 121

QY 161 YSSAIGPYKGLRFPSPVNSLIMKFLAEOIFKNSLTLLPMGGKGSDFPKKSDAEV 220
DB 122 YSSAIGPYKGLRFPSPVNSLIMKFLAEOIFKNSLTLLPMGGKGSDFPKKSDAEV 181

QY 221 MRFOCSFMTLQRIHSYQDVPAAGDIGVAREIGYLFQYKRIITKNYTVGLTPKQGEYGG 280
DB 182 MRFOCSFMTLQRIHSYQDVPAAGDIGVAREIGYLFQYKRIITKNYTVGLTPKQGEYGG 241

QY 281 SEIRPATGAVGVFVENVLKDGESLKGKRCIVSGAGNVAQCAELLEKGAIVLSLSD 340
DB 242 SEIRPATGAVGVFVENVLKDGESLKGKRCIVSGAGNVAQCAELLEKGAIVLSLSD 301

QY 341 SQGYVPEPNGFTRELQAVQDMKKNSARISEYKSDTAAYVGGRRKPEWLDQVDIAFP 400
DB 302 SQGYVPEPNGFTRELQAVQDMKKNSARISEYKSDTAAYVGGRRKPEWLDQVDIAFP 361

QY 401 CATONEIDEHDAELLIKHGCOYVEGANMPSSTNEAIHKYNKAGIICPGKAANAGVAVS 460
DB 362 CATONEIDEHDAELLIKHGCOYVEGANMPSSTNEAIHKYNKAGIICPGKAANAGVAVS 421

QY 461 GLENTORMSLNTWREVRDLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAV 520
DB 422 GLENTORMSLNTWREVRDLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAV 481

QY 521 KAOGAV 526
DB 482 KAOGAV 487

RESULT 7
US-09-070-844-26
Sequence 26, Application US/09070844
Patent No. US20020062495A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanichik & Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-070-844-26

Query Match 90.6%; Score 2465; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 4,8e-213;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 MDATGDTALQKAVKQMATAGTEGLVHGINKPDVROLTLTEIFMKDEQEFMOAVREV 110
DB 1 MDATGDTALQKAVKQMATAGTEGLVHGINKPDVROLTLTEIFMKDEQEFMOAVREV 60

QY 111 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGRVQYSSAIGPYK 170
DB 61 AVSLQPVFEKRPPELLPIFKQIVBERVITFRVSWLDDAGNLQVNRGRVQYSSAIGPYK 120

QY 171 GLRHPSPVNSLIMKFLAEOIFKNSLTLLPMGGKGSDFPKKSDAEVMRFOCSFMTL 230
DB 121 GLRHPSPVNSLIMKFLAEOIFKNSLTLLPMGGKGSDFPKKSDAEVMRFOCSFMTL 180

QY 231 LQRIHSYQDVPAAGDIGVAREIGYLFQYKRIITKNYTVGLTPKQGEYGSSEIRPEATGY 290
DB 181 LQRIHSYQDVPAAGDIGVAREIGYLFQYKRIITKNYTVGLTPKQGEYGSSEIRPEATGY 240

QY 291 GAVLFEVENVLKDGESLKGKRCIVSGAGNVAQCAELLEKGAIVLSLSDSQGYVEPNG 350
DB 241 GAVLFEVENVLKDGESLKGKRCIVSGAGNVAQCAELLEKGAIVLSLSDSQGYVEPNG 300

QY 351 FTREQLQAVQDMKKNSARISEYKSDTAAYVGGRRKPEWLDQVDIAFCATONEIDEH 410
DB 301 FTREQLQAVQDMKKNSARISEYKSDTAAYVGGRRKPEWLDQVDIAFCATONEIDEH 360

QY 411 DAEILLIKHGCOYVEGANMPSSTNEAIHKYNKAGIICPGKAANAGVAVSGLLENTORMS 470
DB 361 DAEILLIKHGCOYVEGANMPSSTNEAIHKYNKAGIICPGKAANAGVAVSGLLENTORMS 420

QY 471 LNTWREVRDLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAOGAV 526
DB 421 LNTWREVRDLERIMKDIYDSAMGSPRRYVNDLAAGANIAGFTKVADAVKAOGAV 476

RESULT 8
US-10-627-886-26
Sequence 26, Application US/10627886
Publication No. US20040128710A1
GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.
MILLER, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 26:
LENGTH: 476 amino acids
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-627-886-26
Query Match 90.6%; Score 2465; DB 16; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.8e-213;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51 MDATTGDTALQKAVKQMATKAGTEGLVHGIXNPDVRLQLTEIFMKDPEOQEFMQAVREV 110
DB 1 MDATTGDTALQKAVKQMATKAGTEGLVHGIXNPDVRLQLTEIFMKDPEOQEFMQAVREV 60
QY 111 AVSLQPVFERKPELLPIFKQIVPEERYITFRVSWLDAGNIQVNRGRVYSSAIGYK 170
DB 61 AVSLQPVFERKPELLPIFKQIVPEERYITFRVSWLDAGNIQVNRGRVYSSAIGYK 120
QY 171 GLRHPSPVNSIMKFLAFOIFKNSLTLLPMGGGSGSDPDKKSDAIVARFCQSPMTE 230
DB 121 GLRHPSPVNSIMKFLAFOIFKNSLTLLPMGGGSGSDPDKKSDAIVARFCQSPMTE 180
QY 231 LQRIHSYVQDVPADIGVAREIGYLFQGYKRIKNTYGVLTTPKGOEYGSSEIRPEATGY 290
DB 181 LQRIHSYVQDVPADIGVAREIGYLFQGYKRIKNTYGVLTTPKGOEYGSSEIRPEATGY 240
QY 291 GAVLFVENVTLKDKESLKGKRCVSGAGNVAQYCAELLLEGAIVLSLSDSGYVYPNG 350
DB 241 GAVLFVENVTLKDKESLKGKRCVSGAGNVAQYCAELLLEGAIVLSLSDSGYVYPNG 300
QY 351 FTREQLAVQDMKKKNSARISEYKSDTAVVGDPRKPMELDCQVDIAFPQATONEIDH 410
DB 301 FTREQLAVQDMKKKNSARISEYKSDTAVVGDPRKPMELDCQVDIAFPQATONEIDH 360

QY 411 DAELLIKGCGQYVEGANMSTNEAIHKYKAGIITPCGAANAAGVAVSGLEMTONRMS 470
DB 361 DAELLIKGCGQYVEGANMSTNEAIHKYKAGIITPCGAANAAGVAVSGLEMTONRMS 420
QY 471 LMTREVRDKLERIMDIYDSAMGPRRRNVVLAAGANTAGTXYADAKAGAV 526
DB 421 LMTREVRDKLERIMDIYDSAMGPRRRNVVLAAGANTAGTXYADAKAGAV 476
RESULT 9
US-10-282-122A-66687
Sequence 66687, Application US/10282122A
Publication No. US2004029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 66687
LENGTH: 445
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66687
Query Match 48.1%; Score 1309; DB 15; Length 445;
Best Local Similarity 59.2%; Pred. No. 7.3e-109;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
QY 86 VRQLLEIFMKDPEOQEFMQAVREVAISLOPVEKPELLP--IFKQIVPEERYITFRVS 143
DB 5 VDAFLERLKRDDQDFEFOHAEVLRSLMPELEANPHYLEAGITIEIVPEERAILFRVP 64
QY 144 WLDDAGNLQVNRGFRVYSSAIGPYGGLRFHPSVNI,SIKFLAFOIFKNSLTLLPMGG 203
DB 65 WVDQDGRVNRGRVYRQMSAIGPYGGLRFHPSVNLGVLFKFLAFOVFNLSLTLLPMGG 124
QY 204 GKGGSDPDKKSDAIVARFCQSPMTELORIHSYVQDVPADIGVAREIGYLFQGYKRI 263

```

Db      125 GKGSGDPDPKSGDAEVMRFQCSFMSELRYHVADLDPVPAIDIGVAREIGYLFQYKRL 184
Qy      264 TKNTGVTLPKQDGYGSEIRPEATGYGAVLFVENVLKDQKESLKGRCCLVSGAGNVAQ 323
Db      185 SNOGTSVLTGSGYSGSLIRPEATGFCVFADEMUKDRGRGDRVALISGSGNVAQ 244
Qy      324 CAEELLKGAIVLSLSQGYVYEPNGFTREQLQAVODMKKNSARISEYKSDTAAYVG 383
Db      245 AARVMEMGKIVLSDSSEGLVLAAGLSDEQWETLWELKVR-RGIRMAEQPSIQFL 303
Qy      384 DRRKPELDCQVDIAFPQATONEIDEHDAELLIRHGCQYVVGAMPSSTNEAIHKYNK 443
Db      304 EGRFPWGLAC--DIALPCATQNEIDAEADARLLANGCVVAGANMSTLEAVDLFLAAG 361
Qy      444 ILYPGKAAAGVAVSGLENTQRMSLNWTREVRDKLERIMDIYDSA-MGFSRYNV 502
Db      362 ILVAPGASNAAGVAVSGLEMSQNAMRLRWSEGEVDTLHGMQSIHHAICLLYEEQGRV 421
Qy      503 DLAAGANIAGFTKVAADAVKAQAV 526
Db      422 NYVGANIAGFVKVADAMLAQGV 445

```

RESULT 10

US-10-282-122A-65129

Sequence 65129, Application US/10282122A

Publication NO. US20040029129A1

GENERAL INFORMATION:

```

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Treawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65129
LENGTH: 444
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65129

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Query Match 47.7%; Score 1297.5; DB 15; Length 444;
 Best Local Similarity 57.4%; Pred. No. 7,9e-108;
 Matches 257; Conservative 70; Mismatches 106; Indels 15; Gaps 6;

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Qy      85 DVNQLTEIFMKDPEQGEFMAVREAVASLQPVFEKRPBELL--PIFQIYEPERVITFRV 142
Db      3 DLNLTFLANLKQRBNQPFPHQAVEVFMSSLDPLAKNPXYTQOSLIERIVPERVAFVRV 62
Qy      143 SMVDDAGNLQVNGFRQYQSSAIGPYKGRFRHPSVNLSTMKFLAFQIRKNSLTTLPMG 202
Db      63 TWDDKQGVQVNGYRQVMSAIGPYKGRFRHFTYDLGVLFKFLAFQVFNKALTTLLPMG 122
Qy      203 GKGSGSPDPKSGDAEVMRFQCSFMTELORHISYVDVAGDVGAREIGYLFQYK 262
Db      123 GKGSGSPDPKSGDAEVMRFQCFMTLIRHICADTDVAGDVGAREIGYLFQYK 182
Qy      263 ITKNYTVLTPKQDGYGSEIRPEATGYGAVLFVENVLKDQKESLKGRCCLVSGAGNVAQ 322
Db      183 IRNEFTSVLTGKGLWEGSLIRPEATGCVYFAQMLQTRNDSFEKRVILISGSGNVAQ 242
Qy      323 YCAEELLKGAIVLSLSQGYVYEPN-GFTREQLQAVQDMKKNSARISEYKSDTAAY 381
Db      243 YAAEKALQLGAKVLTVSDSDGFVLPDIGNTEQLAALIELKEVRRE-RVATYAKEQGLQ 301
Qy      382 VGBRRKPELDCQVDIAFPQATONEIDEHDAELLIRHGCQYVVGAMPSSTNEAIHKYNK 441
Db      302 YFENQKPMGV--AAEILPCATQNEIDAEAKTILANGCVVAGANMSTLEAVEQPIK 359
Qy      442 AGIILYCPKAAAGVAVSGLENTQRMSLNWTREVRDKLERIMDIYDSAMGPSRY 500
Db      360 AGILYAPGASNAAGVAVSGLEMSQNAMRLRWSEGEVDTLHGMQSIHHSCL---KYG 415
Qy      501 ----NDLAAGANIAGFTKVAADAVKAQ 524
Db      416 KVGDKNVYVVGANIAGFVKVADAMLAQ 443

```

RESULT 11

US-10-282-122A-66041

Sequence 66041, Application US/10282122A

Publication NO. US20040029129A1

GENERAL INFORMATION:

```

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Treawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931

```



```

Db      74  WVDQGVNVRGRVEXNSAIGPYKGLRPHPSVYLGIIFKLGFEQIFKNSLTGLPIGG 133
Qy      204  GKGSDFDPKKGDAFVWRFCQSPMTLORHISVVDVPAGDIGVAREIGYLFQYKRI 263
Db      134  GKGSDFDPKKGSEGEIMFCQSPITELRYLGADTDVPAGDIGVAREIGYLFQYKRI 193
Qy      264  TKNYTGVLTTPKQEVGSGSEIRPEATGYGAVLFVENVLKDKGESLKGKCLVSGANVAQY 323
Db      194  TNRVEGVLTGKGLTFGSGISGTEATGYGLVFMELKAVGKSPSGATVVSNGNVAIY 253
Qy      324  CAELLLEKGAIVLSLDSQGYVEPNNGFTREQLQAVODMKKNNSARISEYKS--DTAVY 381
Db      254  ATQKATQLGGVVAMSDSNGIYIDKGINLDTVRQLKEVERK---RLKDYVSIHPTAEY 309
Qy      382  VGDRKXPMELDCQVDIAFPACATONEIDEHDAELLIKHGQYVVEGAMPSTNEAIIHKYK 441
Db      310  YEGCAGIWTIICA--IALPCATONEIDGAAEVLKNGCTAVGEGANNPSTPEAVDVFLQ 367
Qy      442  AGIITYCPGKAMAGVAVSGLMTOHRMSLMTREEVYDKLERIMKDIYDSAMGPSRRYN 501
Db      368  HKIITYGPKAMAGVAVSALEMSQNSRVSMTPEEVDAKLKINIMVNIYHNSKAAQEPG 427
Qy      502  VD--LAAGANITAGFTKVADAVKAQAV 526
Db      428  FEGNLVAGANITAGFLKVAEAMKAQTV 454

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Search completed: July 9, 2005, 18:39:34
 Job time : 168 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 18:25:38 ; Search time 42 Seconds
(without alignments)
1205.000 Million cell updates/sec

Title: US-10-627-886-2

Perfect score: 2720

Sequence: 1 MOTALVAKPIVAAPLAPR.....GANIAGFTKVADAVKAGAV 526

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2488.5	91.5	523	1 S17949	glutamate dehydrog
2	1324.5	48.7	449	1 A62489	glutamate dehydrog
3	1309	48.1	445	2 H83072	glutamate dehydrog
4	1300.5	47.8	444	2 H81050	glutamate dehydrog
5	1294.5	47.6	444	2 H81825	glutamate dehydrog
6	1238	45.5	449	2 A64053	glutamate dehydrog
7	1214.5	44.7	444	2 T10487	glutamate dehydrog
8	1214	44.6	448	2 D98019	glutamate dehydrog
9	1212	44.5	448	2 H95151	glutamate dehydrog
10	1210.5	44.5	458	2 H83912	NADP-specific glut
11	1205.5	44.3	424	2 E75362	glutamate dehydrog
12	1201	44.2	447	1 DEECN	glutamate dehydrog
13	1199	44.1	443	2 F66990	NADP-specific glut
14	1198	44.0	447	2 C90937	NADP-specific glut
15	1198	44.0	447	2 G85785	NADP-specific glut
16	1189.5	43.7	458	2 A11503	NADP-specific glut
17	1185	43.6	447	2 S32237	glutamate dehydrog
18	1182	43.5	447	1 A33504	glutamate dehydrog
19	1181	43.4	447	2 AF0710	glutamate dehydrog
20	1180.5	43.4	458	2 A11144	NADP-specific glut
21	1153	42.4	447	2 A60483	glutamate dehydrog
22	1150	42.3	448	2 D64567	glutamate dehydrog
23	1143	42.0	450	2 S22403	glutamate dehydrog
24	1142.5	42.0	448	2 B95277	probable glutamate
25	1139	41.9	448	2 F71862	glutamate dehydrog
26	1133.5	41.7	446	2 S06938	glutamate dehydrog
27	1121.5	41.2	454	1 DENCN	glutamate dehydrog
28	1115.5	41.0	459	1 S04904	glutamate dehydrog
29	1109	40.8	457	2 S63608	glutamate dehydrog

30	1092	40.1	451	2 T41492	probable glutamate
31	1067.5	39.2	459	2 S17975	glutamate dehydrog
32	1037.5	38.1	454	1 A25275	glutamate dehydrog
33	1022	37.6	457	2 S51960	glutamate dehydrog
34	997.5	36.7	624	2 B96556	hypothetical prote
35	579.5	21.3	416	2 T45284	glutamate dehydrog
36	576.5	21.2	416	2 G72305	glutamate dehydrog
37	557	20.5	424	2 A70055	glutamate dehydrog
38	552.5	20.3	421	2 F83852	glutamate dehydrog
39	545.5	20.1	426	2 G69933	glutamate dehydrog
40	544.5	20.0	414	2 G89862	NAD-specific gluta
41	536	19.7	372	2 G84220	glutamate dehydrog
42	530	19.5	420	2 D75176	glutamate dehydrog
43	529.5	19.5	430	2 F83989	glutamate dehydrog
44	527.5	19.4	420	2 F84142	glutamate dehydrog
45	527.5	19.4	421	2 B81079	glutamate dehydrog

ALIGNMENTS

RESULT 1

glutamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fsegment)
N/Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C/Species: Chlorella sorokiniana
C/Date: 30-Jun-1992 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C/Accession: S17949; S17950; S19030
R/Cock, J.M.; Kim, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R.
Plant Mol. Biol. 17, 1023-1044, 1991
A/Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP
A/Reference number: S17949; MUID:9203762; PMID:1178478
A/Accession: S17949

A/Molecule type: DNA
A/Residues: 1-523 <COC>
A/Cross-references: UNIPROT:P28998; EMBL:X58831
A/Accession: S17950
A/Molecule type: mRNA
A/Residues: 1-523 <COC2>
A/Cross-references: EMBL:X58832; NID:G18272; PIDN:CAA41636.1; PID:G18273
R/Schmidt, R.R.
submitted to the EMBL Data Library, April 1991
A/Reference number: S19030
A/Accession: S19030
A/Molecule type: DNA
A/Residues: 1-219, 'LW', 222-523 <SCH>
A/Cross-references: EMBL:X58831
C/Genetics:
A/Genome: nuclear
A/Introns: 6/2; 29/1; 40/3; 56/3; 85/3; 127/3; 149/3; 175/1; 183/3; 211/1; 246/1; 272/2;
C/Superfamily: glutamate dehydrogenase (NAD(P)+)
C/Keywords: chloroplast; hexamer; NADP; oxidoreductase
F/202/Binding site: substrate (Lys) #status predicted

Query Match	91.5%	Score 2488.5	DB 1	Length 523
Best Local Similarity	95.7%	Pred. No. 3.2e-175		
Matches 488	Conservative	4	Mismatches 13	Indels 5
Gaps 2				
Qy	17	ARPECLAPMPCAWMSAKRDVRAKAVSLEEQISAMDATTDFTALQAVKQMATKAGTEG	76	
Db	19	ALPRAVA---CAGRSKKRDVAAK--RLRSRSPMDTTDDFTALQAVKQMATKAGTEG	73	
Qy	77	LVIHGKIPDVRLTLTEIFMKDPEQOEPMQAVREVAVSLQPFEXRPELLPIPKQIVPER	136	
Db	74	LVIHGKIPDLRLTLTEIFMKDPEQOEPMQAVREVAVSLQPFEXRPELLPIFKQIVPER	133	
Qy	137	VITPRVSWLDAGNLQVNRGFRVQYSALIGPYGGJLRFHPSVNLSTIKPLAFQIFQNSL	196	
Db	134	VITPRVSWLDAGNLQVNRGFRVQYSALIGPYGGJLRFHPSVNLSTIKPLAFQIFQNSL	193	
Qy	197	TTLPFMGGKSGSDFDPKGSDAEMRFQSGFMTLQRIHSYVDVPAQDVGARREIGYL	256	
Db	194	TTLPFMGGKSGSDFDPKGSDAEMRFQSGFMTLQRIHSYVDVPAQDVGARREIGYL	253	

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Qy 257 FGQYKRTKNTYGVLPKGOEYGSSEIRPEATYGAVLFEVENVLKDGESLKGRCCLVSG 316
D 254 FGQYKRTKNTYGVLPKGOEYGSSEIRPEATYGAVLFEVENVLKDGESLKGRCCLVSG 313
Qy 317 AGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVDMKKKNSARISEYKS 376
D 314 AGNVAQYCAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVDMKKKNSARISEYKS 373
Qy 377 DTAYVVDNRKRWELDCQVDIAFPCCATONEIDEHDAELLKHGGOYVVEGANNPSTNEAI 436
D 374 DTAYVVDNRKRWELDCQVDIAFPCCATONEIDEHDAELLKHGGOYVVEGANNPSTNEAI 433
Qy 437 HKYKAGIITPCGKAANAGVAVSGLEMTQNRMSLNTREEVROKLBRIIMKDIYDSAMGP 496
D 434 HKYKAGIITPCGKAANAGVAVSGLEMTQNRMSLNTREEVROKLBRIIMKDIYDSAMGP 493
Qy 497 SRRYVNDLAAGANIAGFTKVAADAVKAQAV 526
D 494 SREYVNDLAAGANIAGFTKVAADAVKAQAV 523
```

RESULT 2

```
A42489
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Giardia lamblia
N:Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C:Species: Giardia lamblia
C>Date: 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A42489
R:Yee, J.; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
A:Title: Isolation and characterization of a NADP-dependent glutamate dehydrogenase gene
A:Reference number: A42489; MUID:922181410; PMID:1559991
A:Accession: A42489
A:Molecule type: DNA
A:Residues: 1-449 <YEE>
A:Cross-references: UNIPROT:P28724; GB:M64604; NID:G159108; PIDN:AAA29155.1; PID:G159108
A:Note: Sequence extracted from NCBI backbone (NCBIIN:94071, NCBIIP:94074)
C:Superfamily: glutamate dehydrogenase (NAD(P)+)
C:Keywords: NADP; oxidoreductase
F:135/Binding site: substrate (Lys) #status predicted
```

```
Query Match 48.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 1.2e-89;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5;

Qy 86 VRQLITEIFMKDPEQGFMAVREAVNSLOPVEKRPBLLP--IFQIYPEREVTFRVSWL 145
D 6 IEELIAVIKORDEGHTFRRQAVEEVVSLKVIIFEREKPIPIFERMLEPERVITFRVPM 65
Qy 146 DDAGNLQVNRGFRVQYSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTTLPMGGK 205
D 66 DDARIVNNGFRVQYNSALGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTTLPMGGK 125
Qy 206 GGSDFDPKGSDAEVMFRCOSFMTELQRIHSYVDVPAAGDIGVAREIGYLFQGYKRTK 265
D 126 GGSDFDPKGSNDNVMFRCOSFMTELQRIHVAADTDVARGDIGVAREIGYLFQGYKRLRN 185
Qy 266 NYTVGLTPKGOEYGSSEIRPEATYGAVLFEVENVLKDGESLKGRCCLVSGANVAQYCA 325
D 186 EFTVLTQKRVKMGSGFIRPEATYGAVLFEVENVLKDGESLKGRCCLVSGANVAQYCA 245
Qy 326 ELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVDMKKKNSARISEYKS--DTAVVY 382
D 246 EKLQIDAKVLTFTSDSGYVYEPNGFTREQLQAVDMKKKNSARISEYKS--DTAVVY 304
Qy 383 GDRKKPWE-LDCQYDIAPPCATONEIDEHDAELLKHGGOYVVEGANNPSTNEAIHKYKN 441
D 305 G--KKPWECPGQNDICMPCATQNEHVGDDATRLVGLGKFAAGANMPSTNEAIVHYHA 362
Qy 442 AGIITPCGKAANAGVAVSGLEMTQNRMSLNTREEVROKLBRIIMKDIYDSAMGPSRRYN 501
D 363 KGVAVYCPAKSNAGVAVSGLEMTQNRMSLNTREEVROKLBRIIMKDIYDSAMGPSRRYN 422
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```
Qy 502 --VDLAAGANIAGFTKVAADAVKAQAV 526
D 423 HPKNYQMGANIAGFTKVAADAVKAQAV 449
```

RESULT 3

```
H83072
glutamate dehydrogenase PA4588 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brum, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: H83072
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:Cross-references: UNIPROT:Q9HVJ7; GB:AE004872; GB:AE004091; NID:99950829; PIDN:AA07976
A:Experimental source: strain PA01
C:Genetics:
A:Superfamily: glutamate dehydrogenase (NAD(P)+)
```

```
Query Match 48.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 1.6e-88;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
```

```
Qy 86 VRQLITEIFMKDPEQGFMAVREAVNSLOPVEKRPBLLP--IFQIYPEREVTFRVSWL 143
D 5 VDAFLERLKRDDQDFEFGHVAEEVRLSLMFLFANPHYIEAGIIRIVEPERAILFRVP 64
Qy 144 WLDDAGNLQVNRGFRVQYSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTTLPMGG 203
D 65 WLDDQGRVNRGFRVQYSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTTLPMGG 124
Qy 204 GKSDFDPKGSDAEVMFRCOSFMTELQRIHSYVDVPAAGDIGVAREIGYLFQGYKRTK 263
D 125 GKSDFDPKGSDAEVMFRCOSFMTELQRIHVAADTDVARGDIGVAREIGYLFQGYKRL 184
Qy 264 TKQYVGLTPKGOEYGSSEIRPEATYGAVLFEVENVLKDGESLKGRCCLVSGANVAQY 323
D 185 SNQFTSVLTGKLSYGSGLIRPEATYGAVLFEVENVLKDGESLKGRCCLVSGANVAQY 244
Qy 324 CAELLLEKGAIVLSLSDSGYVYEPNGFTREQLQAVDMKKKNSARISEYKSDTAVVY 383
D 245 AAKVWEMGSKVLSLSDSGYVYEPNGFTREQLQAVDMKKKNSARISEYKSDTAVVY 303
Qy 384 DRRKRWELDCQYDIAPPCATONEIDEHDAELLKHGGOYVVEGANNPSTNEAIHKYKN 443
D 304 EGRRPWGLAC--DIAFPCCATQNEHDAEDARLLANGCVCAEAGANMPSTNEAIDLFL 361
Qy 444 IITPCGKAANAGVAVSGLEMTQNRMSLNTREEVROKLBRIIMKDIYDSAMGPSRRYN 502
D 362 ILVAPGASVAGVAVSGLEMTQNRMSLNTREEVROKLBRIIMKDIYDSAMGPSRRYN 421
Qy 503 DLAAGANIAGFTKVAADAVKAQAV 526
D 422 NYVKGANIAGFTKVAADAVKAQAV 445
```

RESULT 4

```
H81050
glutamate dehydrogenase, NADP-specific NMB1710 [imported] - Neisseria meningitidis (strain H81050)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
```

Query Match 47.6%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 1.9e-87;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

QY DVRLTLRIEIPKDEQOEPMQAVEAVSLQPVFEKPELL--PIFKIYVPERVITFRV 142
DB DLNTLTPANLKORNNQSEPFHOAVEEPMSLDPLAKPKYTKQSLERIVEPERVWFRV 62
QY 143 SWLDDAGNLQVNRGFRVQYSSAIGPYKGLRFPHPVSLSIMKFLAFEQIFKNSITLTPMG 202
DB 63 TWODDKQOVQNRRIYRQMSAIGPYKGLRFPHPVSLSIMKFLAFEQIFKNSITLTPMG 122
QY 203 GKGSGDPDPKSGSDAEVWRFQSFMTLQRHISYVODVPAGDIGVAGREIGYLFQYKR 262
DB 123 GKGSGDPDPKSGSDAEVWRFQSFMTLQRHISYVODVPAGDIGVAGREIGYLFQYKR 182
QY 263 ITRKYTVGLTPKQGVGSGSELRPAATGYGAVLPYENVLXKQGBSLKRCGLVSGAGVAAQ 322
DB 183 ITRNFSSVLTKGKLEWGSGLRPEATGYGCVYPAQNALQTRNDSFEKRLVLSGSGVAAQ 242
QY 323 YCALLELEKGAIVLSLDSOGYVEP--NGFTREQLQAVQOMKKKNSARISEYSDPAVY 381
DB 243 YAAEKALQLGAKVLTVDSDNGFVLPDPSGSENAQALILEKVRRE--RAATAKEGLQ 301
QY 382 VGDRRKWEMLDQVDIAFPCATONEIDEHDAELLIKHCOYVVEGAMPSTNEAHRKYN 441
DB 302 YFENQKPMGV--AAEIALPCATQNEIDEEAKTLLANGCVYVABGAMPSTLGAVEQFIK 359
QY 442 AGIITYCGKAAAGGVAVSGLEMTQRNMSLMTWRETRDGLERIMDIYTSAMGPSRY- 500
DB 360 AGIITYCGKAAAGGVAVSGLEMTQRNMSLMTWRETRDGLERIMDIYTSAMGPSRY- 415
QY 501 ----NVDLAAGANAGFTKVAADAVKAG 524
DB 416 KVGDTVTVYVNGANAGFTKVAADAVKAG 443

RESULT 6
A64053
glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Haemophilus influenzae (strain Rd KM20)
C1Species: Haemophilus influenzae
C1Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C1Accession: A64053
R1Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirsnes, E.F.; Kerlavage, A.
D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A1Authors: Gnehm, C.J.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter,
A.L.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A1Reference number: A64000; MUID:95350630; PMID:7542800
A1Accession: A64053
A1Status: nucleic acid sequence not shown; translation not shown
A1Molecule type: DNA
A1Residues: 1-449 <TRIGR>
C1Superfamily: glutamate dehydrogenase (NAD(P)+)
C1Keywords: NADP; oxidoreductase

Query Match 45.5%; Score 1239; DB 2; Length 449;
Best Local Similarity 55.6%; Pred. No. 2.8e-83;
Matches 247; Conservative 64; Mismatches 117; Indels 16; Gaps 5;

QY 90 LTELFMKDPDQOEPMQAVEAVSLQPVFEKPELL--PIFKIYVPERVITFRVSLDD 147
DB 11 LTKVAGQRDGYQPEFLQAVREVFTSIMPFLANKRYSBALERLVEBERAFQFRVAMTDD 70
QY 148 AGNLQVNRGFRVQYSSAIGPYKGLRFPHPVSLSIMKFLAFEQIFKNSITLTPMGCGKGG 207
DB 71 KGVQGVNRRARVQPNASIGPFKGMRFHPVSNLSIKFLGFEQIFKNSITLTPMGCAKGG 130
QY 208 SDPDPKSGDAEVWRFQSFMTLQRHISYVODVPAGDIGVAGREIGYLFQYKRITTKYV 267

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Db      13  SDPDPKGSKDAEVMRCQQLMAMELYRHVGADITDPBAGDVGIGREHVEVGLGYMKKLSNGS 190
Qy      268  TGVLTREKGEDEYGGSEELRPBRTGYGAVLPEBENVLKHKGESLKGKCLYSGAGNVAQYCAEL 327
Db      191  ACVFETRGISFGGSLILRPBRTGGLIYFQAMLEKGDSPFGKVVSVSGSGNVAQYVIEK 250
Qy      328  LLEKGAIVLSLSDSGYVVEEPNGFTREOLQAVQDKKKNNBARISEYKSDPAVVGDRRK 387
Db      251  ALSIGAKVVTCSDSGSGYVVDPNPGFTTEKKAALFDI-KATKRGKRVMDVAEGQGLYFEGKR 309
Qy      388  PWELEQCVDIAPFCALQNEIDEDDAELLKHGCGYVVEGAMPESTNEIHKYKAGIYYC 447
Db      310  PWEV--QVDALEPFCALQNELELSDQRLKKNVKKVAEGAMPPTEETALLAADVLFG 367
Qy      448  PGKAANAGVAVSGLEMTQNRMSLWNTREEVYDKLERIMKDIYDSAMPSSRY----- 500
Db      368  PGKAANAGVAVTSGLEMAQSQRILVYTAEBVDAQHRITMDLIHANC-----KKYGTIEGQE 423
Qy      501  NVDLAAGANAGFTKYADAVKQAQGS 524
Db      424  NINYVGANVAGFVQVADAMLQAQ 447

```

Query	7	RESULT
T10487	glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola C/Species: Prevotella ruminicola C/Date: 16-Jul-1999 #sequence_revision: 16-Jul-1999 #text_change: 09-Jul-2004 C/Accession: T10487 R/Men, Z.T.; Morrison, M. submitted to the EMBL Data Library, December 1996 A/Reference number: Z17049 A/Accession: T10487 A/Status: preliminary; translated from GB/EMBL/DBJ A/Molecule type: DNA A/Residues: 1-444 <MEN> A/Cross-references: UNIPROT:P95544; EMBL:U82240; NID:g1772844; PID:g1772845 A/Experimental source: Strain B14 C/Genetics: A/Note: gdnA C/Superfamily: glutamate dehydrogenase (NAD(P)+) C/Keywords: NADP; oxidoreductase	
Query Match	44.7%; Score 1214.5; DB 2; Length 444;	
Best Local Similarity	54.9%; Pred. No. 1.5e-81;	
Matches 242; Conservative	73; Mismatches 119; Indels 7; Gaps 4;	
Qy	88 QLTLEIFKDEEQQEFOQMAVREVAVALPVEKEKPEL-LPIFKQIVEPERVITFRVSML 145	Qy
Db	5 EVIEKTLKAKPGQPEYIQAVSQVLGTIBEEYVKHKPEFKAMLIERTLCVPDRILQFRVSMV 64	Db
Qy	146 DDAGNLQVNRGPRROYSSAIGPYKGLAFHFSYNISSIMKPLAFEOIFKNSLTLLPMGGSK 205	Qy
Db	65 DDGNVQVNTLQRYVQHNNAIGPYKGLAFHKSVAASLIKFLAFEOIFKNSLTLLPMGGAK 124	Db
Qy	206 GGSFPDPKGSDDAEVWRFCCOSFMTLQRIISYQVDPVPAQDVGVARREICGLYFGQYKRTTK 265	Qy
Db	125 GGSFDPDPKGSDDMEWRFCCQAFNELYLLIGPDEVPAGDVGVARREICGLYFGQYKRTTK 184	Db
Qy	266 NYTGVLTPKQGEYGGSEIRPEATGYAVLFEVENVLKDGESLKGKRCILVSGAGNVAQYCA 325	Qy
Db	185 QFGILITKGLEFGGSLIRPEATGYGVNYFLIEDMLKTRGESLKGKTVLVSGAGNVAQYTI 244	Db
Qy	326 ELLEKGAIVLSLSQGVYVEPNQFTBEQLQAVDDMKKNNASAIISRYKSDTAVYVQDR 385	Qy
Db	245 EKLQTLQKAPPTCCSSNSGYIYDPDGIIDEKLAFLIMELKNVNR-GRIKIYAEKRYGVKYEN 303	Db
Qy	386 RKPVELDCOVNIAPPCATQNEIDEHDAELLKGGCOYVVEGANMPSSTEAITHKYKAGII 445	Qy
Db	304 ARPW--GKKALIAITCATODEINEAEKTLILANGYFAVSEGANNPTEPAALIKYPODAKIL 361	Db
Qy	446 YCPGKANAGGVAAGLEMTQNRMSLNTVREVRDKLERIMKDIYDSAM--GPSRRVND 503	Qy

Db 362 YCPGASNAGGVAISGLEMSQNSEKLSWTREVDTKLHNIMDEIHANCVKYGTGPEPGYIN 421

QY 504 LAAGNAGFTTKVADAVKAQS 524
|||:|||||:|||||

Db 422 YKGANVAGFMKVAKAMMAQS 442

RESULT 8
 D98019
 glutamate dehydrogenase (NADP) (EC 1.4.1.4) [imported] - Streptococcus pneumoniae (betastrain)
 C|Species: Streptococcus pneumoniae
 C|Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #ext_change 09-Jul-2004
 C|Accession: D98019
 R|Hoising, J.A.; Albom Jr., W.; Arnold, J.; Biassczak, L.; Burgett, S.; DeHoff, B.S.; De
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
 y, P.; Sun, P.M.; Winkler, M.E.
 Y. Bacteriol. 183, 5709-5717, 2001
 A|Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A|Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A|Reference number: A97872; MUID:21429245; PMID:11544234
 A|Accession: D98019
 A|Status: preliminary
 A|Molecule type: DNA
 A|Residues: 1-448 <KUR>
 A|Cross-references: UNIPROT:O8DPG0; GB:AE007311; PIDN:AAK9584.1; PID:G1545813; GSPDB:GK
 C4Genetics:
 A|Gene: gdhA
 C|Superfamily: glutamate dehydrogenase (NAD(P)+)
 C|Keywords: oxidoreductase

Query Match	Similarity	44.6%	Score 1214	DB 2	Length 448
Beet Local	Similarity	55.7%	Pred. No. 1.6e-81		
Matches 248	Conservative	62	Mismatches 127	Indels 8	Gaps 4
QY	86	VRLTLTEIFMKPDEOEFMQAVREAVSLQPVKEKPELLP--IFKQIVERVITRRVS	143		
DB	8	IQSVETVYKARNGHEAEFLQAVVEFNTLEPVEKHPYEIENILARITERVYSFRVP	67		
QY	144	WLDNAGNLQVNRGFRVQISSAIGPYKGIIRFHSVNLSTMKFLAFEOIFKNSLTLPMGG	203		
DB	68	WDRDQKTVQVNRNGYRVQVFNASAVGPYKGIIRFHPVTAQGIILKFLGFEOIFKNVLTGLPIGG	127		
QY	204	GKGSDFDPKGSKDVEVMRFCSFMTELORHIIYVDDVPAGDIGVAREIGVYFGQYKRI	263		
DB	128	GKGSDFDPKGTIDAEVAFCSFMTELQKHIPSIDVPAGDIGVAREIGVYKQYKRL	187		
QY	264	TKNYTGVLTPKQOEGSEIRPEATGYAVLFEVENYLKDKGESLKGRCLVSGAGNAYQY	323		
DB	188	NQFDAGVLTKKPLGFGSLIRPEATGYGLVYIEEMLKANGSFAGKRVVYISGGNAYQY	247		
QY	324	CAELLLEKGAIVLISDSQGYVEPENGFTREQQAQODMKKNNSARISEYKSTAVYVG	383		
DB	248	ALQKTELGAIVISDSNGVYIDENG--DPDLIVDAVEKRR-ARLTAEAAEKATATY	303		
QY	384	DRRKEMELDCQVDIIFPCATONEIDEHDAELLKHGCOVYVEGANGPSTINEALHKYNKAG	443		
DB	304	HEGSWYTAAGNVDIALLPCATONEINEAAKRLVAQGVICVSEBANGPNSNDALKVYKENG	363		
QY	444	IYYCGKAANAGGAVVSGLEMTQNRMSLWMTREEVDFKLERIKMDIYDSAMGSRRYNV	502		
DB	364	IYYGPAKKAANAGGAVVASALEMSQNSLRLSMTREEVDFGRKLDIMTNIENFAKTTSYGLD	423		
QY	503	-DLAAGANAGFTKVAADAVKAQAV	526		
DB	424	KDYLAGANIATAFENVANAMIAQIV	448		

RESULT 9
 H95151
 NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae (strain TIGR4)
 C/Species: Streptococcus pneumoniae
 C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C/Accession: H95151

R;Teteljin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Authors: Lofcus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: H95151

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <KUR>

A:Cross-references: UNIPROT:Q97QB4; GB:AE005672; PIDN:AAK75409.1; PID:g14972791; GSPDB:C

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1306

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.6%; Score 1212; DB 2; Length 448;

Best Local Similarity 55.5%; Pred. No. 2.3e-81;

Matches 247; Conservative 63; Mismatches 127; Indels 8; Gaps 4;

QY 86 VROLTELFMDPEQOFMVAQVAVSLQVFEKRPBLP--IFKQIVBERVITFRVS 143

DB 8 IQSVFETVKANGHEAEFLQAVEEFNTLEBEVFEKHPEYIEENILARITTEBERVVSFRVP 67

QY 144 WLDDAGNLQVNRGRVQVSSAIGYKGGSLRPHSPVNSIMKFLAFOEFKNSLTLPKGG 203

DB 68 WVDNDGKIQVNRGRVQVSSAIGYKGGSLRPHSPVNSIMKFLAFOEFKNSLTLPKGG 127

QY 204 GKGSGSDPDKSGDAEVMRFGQSFMTLORHISYVODPADIGVAREIGYLFQGYKRI 263

DB 128 GKGSGSDPDKSGDAEVMRFGQSFMTLORHISYVODPADIGVAREIGYLFQGYKRI 187

QY 264 TKATYVLTTPKQGYGSGSEIRPEATYGAVL.FVENVLKDGESLKGKRCVSGAGNVAQY 323

DB 188 NQPDAGVLTGKPLGFGSLRPEATYGAVL.VYVTEEMLKANGNSFAGKVVISGSGNVAQY 247

QY 324 CAELLEKSGAVLSLSDQGYVPENGFTREQLQAVQDMKKNSARISEKSDPAVYVG 383

DB 248 ALQVATELGATVSVSDNGVYIDENGL--DFDLVDVKEKR-ARLTTEAARATATY 303

QY 384 DRKRWELDCQVDIAFCATONEIDEHDAELLIKGCOYVEGANMPESTNEAIHKYNAG 443

DB 304 HEGVTVYAGNYDIALCATONEINGEAKRLVAGVYCVSEGANMSDDAIKYKENG 363

QY 444 IYVPGAAAGVAVSGLENTORMSLMTREVRDLERIMKIDYDSAMPSPRRYV- 502

DB 364 IYVPGAAAGVAVSGLENTORMSLMTREVRDLERIMKIDYDSAMPSPRRYV- 502

QY 503 -DLAAGNIAAGTAVDAVKAQAV 526

DB 424 KDYLGAANIATFENVANAMIAQIV 448

RESULT 10

E83912

NADP-specific glutamate dehydrogenase gdhA [imported] - *Bacillus halodurans* (strain C-12)

C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: E83912

R;Takami, H.; Nakaseko, K.; Takaki, Y.; Maeno, G.; Saeaki, R.; Masui, N.; Fuji, F.; Hirz

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: E83912

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-458 <STO>

A:Cross-references: UNIPROT:Q9RB34; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA0058

Query Match 44.5%; Score 1210.5; DB 2; Length 458;

Best Local Similarity 54.7%; Pred. No. 3e-81;

Matches 252; Conservative 71; Mismatches 121; Indels 17; Gaps 7;

QY 77 LVHGKNDPDRQLTEIF---MKDPQOFMVAQVAVSLQVFEKRPBLP--PIFKQ 130

DB 4 LVREKQYVDDQYVQHYETVYKRRNPHEHFAQVKEVPSLLPVLYKHQYVQALLER 63

QY 131 IVEBERVITFRVSWLDDAGNLQVNRGRVQVSSAIGYKGGSLRPHSPVNSIMKFLAFOE 190

DB 64 IVEBERVITFRVSWLDDAGNLQVNRGRVQVSSAIGYKGGSLRPHSPVNSIMKFLAFOE 123

QY 191 IFKNSLTLPKGGSDPDKSGDAEVMRFGQSFMTLORHISYVODPADIGVAREIGYLFQ 250

DB 124 IFKNSLTLPKGGSDPDKSGDAEVMRFGQSFMTLORHISYVODPADIGVAREIGYLFQ 183

QY 251 REIGYLFQYKRIKNT-TEVLTTPKQGYGSGSEIRPEATYGAVL.FVENVLKDGESLKG 309

DB 184 KEIGYMGQYKRRGRGFEAGVLTGKIGYGGSLARKATGYTYFVEEMIKHGFSPAG 243

QY 310 KRCVSGAGNVAQYCAELLEKSGAVLSLSDQGYVPENGFTREQLQAVQDMKKNSA 369

DB 244 STVYVSGGAVSIYAKEMAKQAGKAVACSDSGYVDKNGIDLQTVKRLKEVERK--- 299

QY 370 RISRYKSD--TAVYVGRRRPWLDCQVDIAFCATONEIDEHDAELLIKGCOYVEGA 427

DB 300 RISRYVHEHPAHVYVQCGSGIWSVPC--DIALPATONELDEAATMLANGVAVGEA 357

QY 428 NMPESTNEAIHKYNAGIYVPGAAAGVAVSGLENTORMSLMTREVRDLERIMK 487

DB 358 NMPESTNEAIHKYNAGIYVPGAAAGVAVSGLENTORMSLMTREVRDLERIMK 417

QY 488 DIYDSAMPSPRRYV--DLAAGNIAAGTAVDAVKAQAV 526

DB 418 NIYRESIKABLYEASGNLVGANIAGFVYADAMISHGV 458

RESULT 11

E75362

glutamate dehydrogenase - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: E75362

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Yamacheva, J.C.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: E75362

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-424 <WHI>

A:Cross-references: UNIPROT:Q9RTN9; GB:AE002013; GB:AE000513; NID:g6459484; PIDN:AAI1275

A:Experimental source: strain R1

C:Genetics:

A:Map position: 1

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.3%; Score 1205.5; DB 2; Length 424;

Best Local Similarity 56.2%; Pred. No. 6.3e-81;

Matches 240; Conservative 61; Mismatches 119; Indels 7; Gaps 4;

QY 104 MQAVREYAVSLQVFEKRPBLP--PIFKQIVBERVITFRVSWLDDAGNLQVNRGRVQY 161

DB 1 MQAVREYAVSLQVFEKRPBLP--PIFKQIVBERVITFRVSWLDDAGNLQVNRGRVQY 60

QY 162 SSAIGYKGGSLRPHSPVNSIMKFLAFOEFKNSLTLPKGGSDPDKSGDAEVM 221

DB 61 SSAIGYKGGSLRPHSPVNSIMKFLAFOEFKNSLTLPKGGSDPDKSGDAEVM 120

Qy	222	RFOSFMTLOHHSYVQVDPADPDIGAGAEITLGCQYKRIKXNTGYLTJTKGDEYGS	281
Db	121	RFCCALMTLHRLHGPPTDVPAGDIGGREGVEVLGMKMKLANHMGSAFTGIGLSTYGS	180
Qy	282	EIRBEATGYAVLFENVNLADKGESELGKRCCLVSGAGNVAOYCAELLLEKGAIVLSLDS	341
Db	181	LIRBEATGYGVVYFEVHMLDRDREMEGRLVSVSSGNAQOYAIEKALHGAHVLTASNS	240
Qy	342	QGYVYEENGPFREBLOAVODMKKKNSARISEKSKSTAYVYVGBRRKPEWLEDOVDIAPFC	401
Db	241	GGIYVDEDEGFLTYDCLATVLMDIKNEER-GRVYEDAREVGAEFRPGVAPW--DYPVDVALPC	297
Qy	402	ATONEIDEHDAELLIKHGCOYVEGAMNPSTNEAIHKYNKAGIIYCPGSAANAGVAVSG	461
Db	298	ATONELCADPARTLIAGGVAVVAEGANMPCDLAIAOFAEBAGVLYAPGATNAGVATSG	357
Qy	462	LEMTONMSLNTTPEEVRDKLERIMKDIYOSANGPSRR--YNYDLAAGNINIGFTVADA	519
Db	358	LEMSONQNRSLMTREBYDQRLRSIMSAIHSCLEFYRRPRRHVSYLDGANIAGFYKVATRA	417
Qy	520	VKAQGAIV 526	
Db	418	MREGVVL 424	

```

RESULT 12
DEBECN      glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Escherichia coli (strain K-12)
N/Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase
C/Species: Escherichia coli
C/cdate: 03-Aug-1984 #sequence revision 20-Sep-1984 #text_change 09-Jul-2004
A/Acession: A00382; A22413; A64936
R/McPherson, M.J.; Wootton, J.C
NCBI/Nucleotide Res. 11, 5257-5266, 1983
A>Title: Complete nucleotide sequence of the Escherichia coli gdhA gene.
A/Reference number: A00382; MUID:83272967; PMID:6308576
A/Acession: A00382
A:Molecule type: DNA
A/Residues: 1-447 <MCP>
A/Cross-references: UNIPROT:P00370; GB:X00988; GB:D01615; GB:K00565; NID:g41543; PIDN:CA
R/Vallé, F.; Becerrill, B.; Chen, E.; Seeburg, P.; Heyneker, H.; Bollivar, F.
Gene 27, 193-199, 1984
A>Title: Complete nucleic acid sequence of the glutamate dehydrogenase gene from Escherich
A/Reference number: A22413; MUID:84209849; PMID:6373501
A/Acession: A22413
A:Molecule type: DNA
A/Residues: 1-447 <VAL>
A/Experimental source: strain K12
R/Balther, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
Sci. 277, 1453-1462, 1997
A:A. Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Acession: A64936
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A/Residues: 1-447 <BLAT>
A/Cross-references: GB:A0000271; GB:U00096; NID:g1788058; PIDN:AACT4831.1; PID:g1788059,
A/Experimental source: Strain K-12, Substrains MG1655
C/Genetics:
A/Gene: gdhA
A/Map position: 27 min
C/Superfamily: glutamate dehydrogenase (NAD(P)+)
C/Keywords: homohexamer, NADP, oxidoreductase
F_128/Binding site: Substrate (lys) #status predicted

Query March          44.2%; Score 1201; DB 1; Length 447;
Best Local Similarity 54.0%; Pred. No. 1.5e+80;
Matches 241; Conservative 67; Mismatches 128; Indels 10; Gaps 5;

Ox       86 VRQLLTETFMKDPEQGEFGMAVREYAVSLQVFVEKRDEL--LPIFKQIVDERVTTRVS 143
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db    7 LESFTLNHQKDDPNTERPAQAAREVMITLMFLEONPKYROMSILRLVEREVIORRV 66
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OY 144 HUUDDAGNLOVNRGFRVQVYSATIPRYKGLRPHFSVNSLSTIMKPLAFEDIFKNSLTLTLMPG 203
OY 67 WDDDNQOIVNNAMRWQFSSAIGPYKGMRFHFSVNLSTIKELFEGEPFNALTLTLMPG 126
OY 204 GKGSDFPBGKSDAEVNRFCOSFMTELORHISYVDVPADGICVGAREIGYLFQYKRI 263
Db 127 GKGSDFPBGKSGSEGVNRFCQALMTELYRHLGADTDVPAGDIOVGRELEVGFAMGMKKL 186
OY 264 TKNYTGVLTPKQOEYGSSEIRPEATGYGAVLFEVENVLKDKGBSLKGRCLVSGAGNAOY 323
Db 187 SNNTACVFEGKGLSEFGSGLIRPEATGYGVYFTEAMLKRGMGFEGRVSVSGSNAOY 246
OY 324 CAELLERKCAIYLSLSDSGYVYEPNGFTREOLQAVODMKKNNASARISEYKSDTAVYVG 383
Db 247 ALEKMEFARVITLSDSSGTAVDSGFTPEKKEKARLIEI-KASRDGVADVAIAEFGVLVL 305
OY 384 DRRKFMELDCQVDIAPPCATONEIDEDHAELLKHGCOYVEGANMSTBEAIIKYNKAG 443
Db 306 EGQOQWMSL--PDIALPCATONEIDVDAHQHOLIANGKVAABEGANNPTTIEATLTFQOAG 363
OY 444 IIPCCKAANAGVAVSGLEMTONRMSLNMWTRBEEVDKLERIKMDIYDSAM--GFSRRY 500
Db 364 VLFARCKAANAGVATSGLEMAQNAARLQWKAEKVADARLHHIMLDIHHACVCHGSEGEQT 423
OY 501 NVDLAAGANIAGFTKYADAIVKAQAGAV 526
Db 424 N--YVQGANIAGFVKVADAMLAQVI 447

```

RESULT 13
 P96990
 NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: F96990
 R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
 A:Reference number: A96900; UID:21359325; PMID:21359325
 A:Accession: F96990
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-443 <KUP>
 A:Cross-references: UNIPROT:Q97L29; GB:AE001437; PID:AAK78713.1; PID:g15023619; GSPDB:GN
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0737
 C:Superfamily: glutamate dehydrogenase (NAD(P) +)

Query Match	44.1%;	Score 1199;	DB 2;	Length 443;
Best Local Similarity	54.4%;	Fred. No. 2e-80;		
Matches 242;	Conservative 69;	Mismatches 122;	Indels 12;	Gaps 5;
QY	86	VRQLTLEIFMKDPEQOEFMQAVREVAVALPVEKSPBELT-DIFKOIVEPERYTRFVS	143	
DB	4	LKHVWDDVIAKRNPNBEHFQAVKEVLSLEIVAEKHPHWKDKIFDKIVEPERQIIIRFP	63	
QY	144	WLDPAAGNTQVNRGFRVOYSSAIGPYKGLRFHPSSVNLSTMKFLAFEOIFKNSLTLLPMGC	203	
DB	64	WYDDGEEHINNGFRIQFNSAIGPYKGLRFHPSSVNLSTMKFLAFEOIFKNSLTLLPMGC	123	
QY	204	KGKGSDFDPKSGSDAEVWVFCQSPMTELRHISLYVDVPAADIGVGRAREIGYLFGQYKRI	263	
DB	124	KGKGSDFDPKSGSDAEVWVFCQSPMTELRHISLYVDVPAADIGVGRAREIGYLFGQYKRI	183	
QY	264	TKNYTGVLTLPKQOEYVGSSEIRPEATGYGAVLFEVENVLKQGESLKGKRCIVSGAGNVAQY	323	
DB	184	RNESTGVLTLPKQOEYVGSSEIRPEATGYGAVLFEVENVLKQGESLKGKRCIVSGAGNVAQY	243	
QY	324	CABLLLEKCAIYLSLDSGGYTYEPENGFTREQLQAVQDMKKKNSARISYKS--DVAAY	381	

Db 244 ANOKATOLGAKVAMSDSNGYIYDANGININTIRIKIVERK---RIHEXTKHPNASY 299
Qy 382 VGDRRKPELDCQVDIAFPACATONEIDEHDAELIKHGCOYVVEGANMSTNEAIHKYK 441
Db 300 TEGCDGIMKLC--DIALPCATONEIDENSATKTLIANGCVAVGBGANMSTNEAVDLTK 357
Qy 442 AGIYCPGKANAAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKOIYDSAMGSPSRRYN 501
Db 358 NKVIFGPAKANAAGVAVSALEMSQNSMRYSMTREVDTKQNMKNIYKCSNAANEYG 417
Qy 502 VD--LAAGANITAGTTKADAVAKAG 524
Db 418 FEDNLVAGANITAGTTKAVKAEAMYSIG 442

RESULT 14

C90937
NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: C90937
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hatlori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: C90937
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-447 <HAV>
A/Cross-references: UNIPROT:O8XDM9; GB:BA000007; PIDN:BA835890.1; PID:G13361934; GSPDB:C
A/Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: EC2467
C/Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.0%; Score 1198; DB 2; Length 447;
Best Local Similarity 53.8%; Pred. No. 2.4e-80;
Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;
Qy 86 VRQLTEIFMKDPEQEFMAVREAVSLQVPEKPEL--LPFKQIVBERVITRRVS 143
Db 7 LESFLNHVQKRDPMQTEFAQVREVMTTLMPELQNPYKRMSLERLVEBERVIOFRVV 66
Qy 144 WLDDAGNLQVNRGRVVOYSSAIGPYKGLRFPSPVNSIMKFLAFEOIFKNSLTLLPMG 203
Db 67 WDDRNQVQNRKRVVFPSSAIGPYKGMFRHPSVNSILKFLGFEQTFKNAITLLPMG 126
Qy 204 GKGSDPDPKGSDAEVMRFQSGFMTELQRIISVQVDPAGDIGVAREIGYLFQYKRI 263
Db 127 GKGSDPDPKGSSEGEVWRFQALMTLRYRLGADTVDPADIGVAREVGFMAKMKL 186
Qy 264 TKNTYGLTPKQGEYGESEIRPEATGYAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 323
Db 187 SNTNACVFTKGLSGFGLIRPEATGYGLVFTFAMLRKHGMGFRKRVSVSSGNAQY 246
Qy 324 CAELLKEKGAIVLSLSDSGYVVEPNQFTREOLQAVODMKKNSARISEKSDTAVYVG 383
Db 247 AIEKAMEFGARVITASDSGTVVDESGETKEKLARLEI-KSSRDGRADYAKFGLVYL 305
Qy 384 DRKPEWLDQVDIAFPACATONEIDEHDAELIKHGCOYVVEGANMSTNEAIHKYKAG 443
Db 306 EGQQPMGVS--PVDIALPCATONEILDVAHQLLANGVAVAEAGANMPTTIEATELFQOAG 363
Qy 444 ILYCPGKANAAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKOIYDSAM--GPSRY 500
Db 364 VLFAPGKANAAGVAVSGLSLEMAQNAARLGWKAKEVDARLHHIMDIHACVEHGBEGQT 423
Qy 501 NVDLAAGANITAGTTKADAVAKAGAV 526
Db 424 N--YVQGANITAGTVKADAMLAQGI 447

RESULT 15
G85785
NADP-specific glutamate dehydrogenase [imported] - Escherichia coli (strain O157:H7, sub
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: G85785
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: G85785
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-447 <STO>
A/Cross-references: UNIPROT:O8XDM9; GB:AE005174; NID:G12515786; PIDN:AAG56747.1; GSPDB:G
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: gdhA
C/Superfamily: glutamate dehydrogenase (NAD(P)+)

Query Match 44.0%; Score 1198; DB 2; Length 447;
Best Local Similarity 53.8%; Pred. No. 2.4e-80;
Matches 240; Conservative 68; Mismatches 128; Indels 10; Gaps 5;
Qy 86 VRQLTEIFMKDPEQEFMAVREAVSLQVPEKPEL--LPFKQIVBERVITRRVS 143
Db 7 LESFLNHVQKRDPMQTEFAQVREVMTTLMPELQNPYKRMSLERLVEBERVIOFRVV 66
Qy 144 WLDDAGNLQVNRGRVVOYSSAIGPYKGLRFPSPVNSIMKFLAFEOIFKNSLTLLPMG 203
Db 67 WDDRNQVQNRKRVVFPSSAIGPYKGMFRHPSVNSILKFLGFEQTFKNAITLLPMG 126
Qy 204 GKGSDPDPKGSDAEVMRFQSGFMTELQRIISVQVDPAGDIGVAREIGYLFQYKRI 263
Db 127 GKGSDPDPKGSSEGEVWRFQALMTLRYRLGADTVDPADIGVAREVGFMAKMKL 186
Qy 264 TKNTYGLTPKQGEYGESEIRPEATGYAVLFVENVLKDGESLKGKRCCLVSGAGNVAQY 323
Db 187 SNTNACVFTKGLSGFGLIRPEATGYGLVFTFAMLRKHGMGFRKRVSVSSGNAQY 246
Qy 324 CAELLKEKGAIVLSLSDSGYVVEPNQFTREOLQAVODMKKNSARISEKSDTAVYVG 383
Db 247 AIEKAMEFGARVITASDSGTVVDESGETKEKLARLEI-KSSRDGRADYAKFGLVYL 305
Qy 384 DRKPEWLDQVDIAFPACATONEIDEHDAELIKHGCOYVVEGANMSTNEAIHKYKAG 443
Db 306 EGQQPMGVS--PVDIALPCATONEILDVAHQLLANGVAVAEAGANMPTTIEATELFQOAG 363
Qy 444 ILYCPGKANAAGVAVSGLEMTQNRMSLMTREBEVDKLERIMKOIYDSAM--GPSRY 500
Db 364 VLFAPGKANAAGVAVSGLSLEMAQNAARLGWKAKEVDARLHHIMDIHACVEHGBEGQT 423
Qy 501 NVDLAAGANITAGTTKADAVAKAGAV 526
Db 424 N--YVQGANITAGTVKADAMLAQGI 447

Search completed: July 9, 2005, 18:35:51
Job time : 43 sec

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 18:24:52 ; Search time 181 Seconds
(without alignments)
1488.142 Million cell updates/sec

Title: US-10-627-886-2
Perfect score: 2720
Sequence: 1 MGTALVAKPTVAPLAPRR.....GANIAGFTKXADAVKAGAV 526

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488.5	91.5	523	1 DHE4_CHLSO	P28998 chlorella s
2	1375	50.6	510	2 Q81LF7	Q81LF7 plasmidium
3	1361	50.0	1203	2 Q7RQ39	Q7RQ39 plasmidium
4	1328	48.8	446	2 Q7YZU9	Q7YZU9 spiroplasma
5	1327.5	48.8	446	2 Q7R3N7	Q7R3N7 giardia lam
6	1324.5	48.7	449	1 DHE4_GILMA	P28724 giardia lam
7	1309	48.1	445	2 Q9HVT7	Q9HVT7 pseudomonas
8	1300.5	47.8	444	2 Q9JY71	Q9JY71 neisseria m
9	1294.5	47.6	444	2 Q9JTS6	Q9JTS6 neisseria m
10	1287.5	47.3	449	2 Q86Q23	Q86Q23 pseudomonas
11	1286.5	47.3	470	2 Q96940	Q96940 plasmidium
12	1286.5	47.3	470	2 Q81LRO	Q81LRO plasmidium
13	1285	47.2	445	2 Q9Z3C4	Q9Z3C4 pseudomonas
14	1284.5	47.2	437	2 Q7YZU7	Q7YZU7 trichomonas
15	1265	46.5	442	2 Q9TXS8	Q9TXS8 plasmidium
16	1264	46.2	442	2 Q9GTK5	Q9GTK5 uncultured
17	1257	46.2	465	2 Q6S143	Q6S143 uncultured
18	1253.5	46.1	536	2 Q7RG75	Q7RG75 plasmidium
19	1250.5	46.0	448	2 Q8G6L0	Q8G6L0 bifidobacte
20	1250.5	46.0	448	2 Q8G6L0	Q8G6L0 bifidobacte
21	1249.5	45.9	447	2 Q6FDM7	Q6FDM7 rumiinoocccu
22	1241.5	45.6	448	2 Q8XK85	Q8XK85 clostridium
23	1240.5	45.6	449	2 Q8E4J6	Q8E4J6 streptococc
24	1239.5	45.6	448	2 Q835G2	Q835G2 enterococcu
25	1238	45.5	449	1 DHE4_HAEIN	P47793 haemophilus
26	1236.5	45.5	449	2 Q8DY77	Q8DY77 streptococc
27	1234	45.4	447	2 Q61083	Q61083 trypanosoma
28	1231.5	45.3	462	2 Q65W57	Q65W57 manheimia
29	1230.5	45.2	449	2 Q8DUL2	Q8DUL2 streptococc
30	1230	45.2	449	2 Q9CPJ4	Q9CPJ4 pasteurella
31	1225.5	45.1	444	1 DHE3_BACIN	P94598 bacteroides

32	1225	45.0	448	2 Q9AIW1	Q9AIW1 streptococc
33	1214.5	44.7	444	1 DHE4_PRRU	P95544 prevotella
34	1214	44.6	448	2 Q8DPG0	Q8DPG0 streptococc
35	1212	44.6	448	2 Q97QB4	Q97QB4 streptococc
36	1210.5	44.5	458	2 Q9K344	Q9K344 bacillus ha
37	1206.5	44.4	447	2 Q7VSN6	Q7VSN6 bordetella
38	1205.5	44.3	424	2 Q9RTN9	Q9RTN9 deinococcus
39	1205.5	44.3	444	2 Q6A081	Q6A081 bacteroides
40	1205.5	44.3	464	2 Q7WEU7	Q7WEU7 bordetella
41	1202	44.2	448	2 Q8KXN9	Q8KXN9 lactobacill
42	1201	44.2	447	1 DHE4_ECOLI	P00370 escherichia
43	1200.5	44.1	446	2 Q6O996	Q6O996 trypanosoma
44	1200	44.1	449	2 Q6AJB1	Q6AJB1 desulfocale
45	1199	44.1	443	2 Q97L29	Q97L29 clostridium

ALIGNMENTS

RESULT 1
DHE4_CHLSO STANDARD; PRT; 523 AA.
ID DHE4_CHLSO
AC P28998;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH) (Fragment).
OS Chlorella sorokiniana.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3076;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92032762; PubMed=1718478;
RA Cook J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.;
RT "A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella sorokiniana.";
RT Plant Mol. Biol. 17:1023-1044(1991).
CC -1- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate + NH(3) + NADPH.
CC -1- SUBUNIT: Homo- and heterohexamer of alpha and beta subunits. Both subunits are encoded by the same gene.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By ammonium.
CC -1- PPM: The N-termini of the alpha and the beta chains are blocked.
CC -1- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X58832; CA41636.1; -.
DR EMBL; X58831; CA41635.1; ALT_SEQ.
DR PIR; S17949; S17949.
DR HSSP; P24295; IADP.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog; 1.
DR Pfam; PF002812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFVDRGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGNASE; 1.
DR Chloroplast; NADP; Oxidoreductase.
KW NON TER
FT ACT SITE 202 202 By similarity.
FT SEQUENCE 523 AA; 57529 MM; A35FE730B5FE7974 CRC64;

Query Match 91.5%; Score 2488.5; DB 1; Length 523;
 Best Local Similarity 95.7%; Pred. No. 2e-161;
 Matches 488; Conservative 4; Mismatches 13; Indels 5; Gaps 2;

QY 17 ARPPCLAPWPCAWRSARAKRDYRAKAVSLSEQISAMDITGDTFLMLQAVKOMATKAGTEG 76
 DB 19 ALPRAVA---CARGRSAKRDVAAK--RLRSRSPMDATGTGDTFLMLQAVKOMATKAGTEG 73
 QY 77 LVHGIKMPDVROLTEIFMKDPEQOEPMQAVREAVASLOPFEKRPPELLPIFKQIVPER 136
 DB 74 LVHGIKMPDLRLQTEIFMKDPEQOEPMQAVREAVASLOPFEKRPPELLPIFKQIVPER 133
 QY 137 VITFRVSWLDAGNLQVNRGFRVQYSSAIGPYKGLRPHBSVNLIMKFLAFEQIFKNSL 196
 DB 134 VITFRVSWLDAGNLQVNRGFRVQYSSAIGPYKGLRPHBSVNLIMKFLAFEQIFKNSL 193
 QY 197 TTLPMGGGKGSDDPRPKGSAPAEYMRFCQSPMTLQRIHSYVQDVPPAGDIGVGAAREIGYL 256
 DB 194 TTLPMGGGKGSDDPRPKGSAPAEYMRFCQSPMTLQRIHSYVQDVPPAGDIGVGAAREIGYL 253
 QY 257 FGQYKRITKNYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSG 316
 DB 254 FGQYKRITKNYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSG 313
 QY 317 AGNVAQYCAELLLEKGAIVLSLSDSGYVVEPNCFTRBQLOAVQDMKKNNASARISEYKS 376
 DB 314 AGNVAQYCAELLLEKGAIVLSLSDSGYVVEPNCFTRBQLOAVQDMKKNNASARISEYKS 373
 QY 377 DTAVYVDRRRPWLDCQVDIAFPQATONEIDEHDAELIYKHGOYVEGANMSTTEAI 436
 DB 374 DTAVYVDRRRPWLDCQVDIAFPQATONEIDEHDAELIYKHGOYVEGANMSTTEAI 433
 QY 437 HKYKAGITGYCPGANAAGVAVSGLEMTONRMSLNTREBVRDKLERIMKIDYDSAMGP 496
 DB 434 HKYKAGITGYCPGANAAGVAVSGLEMTONRMSLNTREBVRDKLERIMKIDYDSAMGP 493
 QY 497 SRRYVNDLAAGANIAGFTKVAADAVKAQAV 526
 DB 494 SRRYVNDLAAGANIAGFTKVAADAVKAQAV 523

RESULT 2
 Q8ILF7 PRELIMINARY; PRT; 510 AA.
 AC Q8ILF7;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Glutamate dehydrogenase, putative.
 GN ORFNames=PF14_0286;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman K.B., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kye S.,
 RA Chan M.S., Nene V., Shalim S.J., Suh B., Peterson J., Angiuoli S.,
 RA Perte M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M., Fairclough A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McPhaden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.;
 RT "genome sequence of the human malaria parasite Plasmodium
 falciparum";
 RL Nature 419:498-511(2002).
 DR EMBL: AE014820; AAN36899.1; -
 DR HSSP: P24295; IAUJ.
 DR GO: GO:0016491; P:oxidoreductase activity; IEA.
 DR GO: GO:0006520; P:amino acid metabolism; IEA.
 DR InterPro: IPR006095; GUFV_dehydrog.

DR InterPro: IPR006096; GUFV_dehydrog_C.
 DR InterPro: IPR006097; GUFV_dehydrog_N.
 DR Pfam: PF00208; GUFV_dehydrog_1.
 DR Pfam: PF02812; GUFV_dehydrog_N; 1.
 DR PRINTS: PR00082; GUFV_dehydrogase.
 DR PROSITE: PS00074; GUFV_dehydrogase; 1.
 SQ SEQUENCE 510 AA; 57343 MW; AC400045297AC64F CRC64;

Query Match 50.6%; Score 1375; DB 2; Length 510;
 Best Local Similarity 60.0%; Pred. No. 2e-85;
 Matches 267; Conservative 66; Mismatches 104; Indels 8; Gaps 5;

QY 86 VROLLEIFMKDEDEQOEFMQAVREAVASLOPVEKRPPELLPIFKQIVPERVITFRVSWL 145
 DB 70 IEELREKVVSKNKNPEFLQAFEEVLSCLKPFKKNVYIGVLNIAEPRIYQFRVPMI 129
 QY 146 DDAGNLQVNRGFRVQYSSAIGPYKGLRPHBSVNLIMKFLAFEQIFKNSLTLTPMGCGK 205
 DB 130 NDKGEHKNNGFRVQYSSVLPYKGLRPHBSVNLIMKFLAFEQIFKNSLTLTPMGCGK 189
 QY 206 GGSDFDPKGSDAEVRFCQSPMTLQRIHSYVQDVPPAGDIGVGAAREIGYLFGQYKRITK 265
 DB 190 GGSDFDPKGSSEVILFKQSPMTNLFRYIGPMTVPAGDIGVGAAREIGYLFGQYKRITK 249
 QY 266 NYTGVLTPKGOEYGSSEIRPEATGYGAVLFVENVLKDGESLKGRCCLVSGAAGVAYCA 325
 DB 250 SPFGVLTGKNIKWGSNSIRAEATGYGAVYFAENVLKDNLNENKCLVSGAGVAYQYLV 309
 QY 326 ELLLEKGAIVLSLSDSGYVVEPNCFTRBQLOAVQDMKKNNASARISEY--KSDTAVYVG 383
 DB 310 ELLLEKGAIVLSLSDSGYVVEPNCFTRBQLOAVQDMKKNNASARISEY--KSDTAVYVG 367
 QY 384 DRRKPEWLDQVQVIAFPQATONEIDEHDAELIYKHGOYVEGANMSTTEAIHKYKAG 443
 DB 368 ENQKPEWNIIP--DIAFPQATONEINENADLFIQNKCMIVEGANMPTIKALHKQKN 425
 QY 444 IIVCPKANAAGVAVSGLEMTONRMSLNTREBVRDKLERIMKIDYDSAMGPSRRY--N 501
 DB 426 IIVCPKANAAGVAVSGLEMTONRMSLNTREBVRDKLERIMKIDYDSAMGPSRRY--N 485
 QY 502 VDLAAGANIAGFTKVAADAVKAQAV 526
 DB 486 VDLAAGANIAGFTKVAADAVKAQAV 510

RESULT 3
 Q7RQ39 PRELIMINARY; PRT; 1203 AA.
 AC Q7RQ39;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Glutamate dehydrogenase.
 GN Name=PY01264;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XN1;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Koo J.T.W., Perte M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalim S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V.,
 RA Cho U.K., Quackenbush J., Sedegah M., Shoab I.A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii";

RL Nature 419:512-519 (2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB010031; EAA20557.1; -
 DR HSSP; P24295; IADP.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006520; P:amino acid metabolism; IEA.
 DR InterPro; IPR005135; Exo_endo_phos.
 DR InterPro; IPR006095; GLFV_dehydrog.
 DR InterPro; IPR006096; GLFV_dehydrog_C.
 DR InterPro; IPR06097; GLFV_dehydrog_N.
 DR Pfam; PF03372; Exo_endo_phos; 1.
 DR Pfam; PF02081; GLFV_dehydrog; 1.
 DR Pfam; PF02812; GLFV_dehydrog_N; 1.
 DR PRINTS; PR00082; GLFV_DEHYDROGENASE.
 DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
 DR SEQUENCE 1203 AA; 13909 MW; DBE1988BD4C21715 CRC64;
 SQ
 Query Match 50.0%; Score 1361; DB 2; Length 1203;
 Best Local Similarity 59.3%; Pred. No. 5.5e-84;
 Matches 264; Conservative 65; Mismatches 108; Indels 8; Gaps 5;
 QY 86 VRQLTEIFMKDPQOEFMQAVREAVSLOPVFEKRPPELLPIFKQIVPERVITFRVSWL 145
 DB 763 IEEMKENVISKNDQHEFLQAFEEVLSTLKFVKNNIIYGLVNLISPEKVIQFRVPMI 822
 QY 146 DDAGNLQVNRGPRVOYSSAIGPYKGLRPHPSVNLSTMKFLAFQIFKNSLTLLPMGGG 205
 DB 823 NDNEHKNRGRVOYSSVGLPYKGLRPHPTVNLSTVKFGEQIFKNSLTLLPMGGG 882
 QY 206 GGSDFDPKKSDAEVRFCQSFMTLQRIHSYQDVPAQDVGAREIGYLFQYKRIT 265
 DB 883 GGSDFDPKKSSENLIFCOSFMDNLRVYIGPNTDIPAGDVGVSREIGYLFQYKRLN 942
 QY 266 NYTGVLTPKQOYSGSEIRPEATGYAVLFEVENVLKDKGSLKGRCLVSGAGNVAQYCA 325
 DB 943 KFESEVLKGNKIMKGSNIRSATGYAVAFENMLSDNBSLKNKTCIVSSGVAQYLV 1002
 QY 326 ELLLEKAVLSLSDQGYVEENGFTRQLOAVQDMKKNSARISEY--KSDTAVYV 383
 DB 1003 EKLLEKAKVLTMSDSGYLLEPNGFTKEQDKDIMEIKVRE-RIKEYLKYSKTAKEF- 1060
 QY 384 DRRKPMELDCQVDIAFPCATONEIDEHDAELLIKHCOYVEGANMPSTNEAIHKYKAG 443
 DB 1061 ENERPMAVPC-DIVFPCATONEITENDADLLINCKCLVEGANMPTHIKAMKLEKNK 1118
 QY 444 ILYCPGKAANAGVAVGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRY--N 501
 DB 1119 ILICPSKAANAGVAVGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRY--N 501
 QY 502 VDLAAGANIAGFTKVADAVKAGAV 526
 DB 1179 TDLVAGANIAGFTKVADSVFEGGL 1203
 RESULT 4
 Q7YZU9 PRELIMINARY; PRT; 446 AA.
 AC Q7YZU9; (TREMBlrel. 25, Created)
 DT 01-MAR-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Glutamate dehydrogenase (Fragment).
 GN Name=gdh;
 OS Spirochete bacterium.
 CC Eukaryota; Diplomonadida; Hexamitidae; Hexamitinae; Spirochete.
 OX NCBI_TaxId=103874;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 50380;
 RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;
 RA Andersson J.O., Roger A.J.;

RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene
 RT transfer within and between prokaryotes and eukaryotes".
 RL BMC Evol. Biol. 3:14-14 (2003).
 DR EMBL; AF533884; AAP83851.1; -
 DR HSSP; P24295; IADP.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006520; P:amino acid metabolism; IEA.
 DR InterPro; IPR006095; GLFV_dehydrog.
 DR InterPro; IPR006096; GLFV_dehydrog_C.
 DR InterPro; IPR06097; GLFV_dehydrog_N.
 DR Pfam; PF02081; GLFV_dehydrog; 1.
 DR Pfam; PF02812; GLFV_dehydrog_N; 1.
 DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
 DR NON TER 1
 SQ SEQUENCE 446 AA; 49309 MW; AEB43D2A1762DB80 CRC64;
 Query Match 48.8%; Score 1328; DB 2; Length 446;
 Best Local Similarity 58.6%; Pred. No. 2.7e-82;
 Matches 262; Conservative 65; Mismatches 110; Indels 10; Gaps 6;
 QY 85 DVKQLTEIFMKDPQOEFMQAVREAVSLOPVFEKRPPELLPIFKQIVPERVITFRVSW 144
 DB 5 DLKXVLLQO---RAHNIEFCQAVNEVDSLVFEEENPKYISVEQLLEPERVIMFRVPM 61
 QY 145 LDAGNLQVNRGPRVOYSSAIGPYKGLRPHPSVNLSTMKFLAFQIFKNSLTLLPMGGG 204
 DB 62 TDDKGEVNIKGRVQYNSALGPYKGLRPHPSVNLSTMKFLAFQIFKNSLTLLPMGGG 121
 QY 205 KGSDFDPKKSDAEVRFCQSFMTLQRIHSYQDVPAQDVGAREIGYLFQYKRIT 264
 DB 122 KGSDFDPKKSSENVRFQSFMTLSRIHQFTDVPADIGVGEIGYLFQYKRIT 181
 QY 265 KNTYGVLTPEKQOYSGSEIRPEATGYAVLFEVENVLKDKGSLKGRCLVSGAGNVAQY 324
 DB 182 NQFTGILTKAVYSGSLIRPEATGYAVYLLNEMMDNDIDDKKVLVSGAGNVAQY 241
 QY 325 AELLLEKAVLSLSDQGYVEENGFTRQLOAVQDMKKNSARISEY--KSDTAVYV 382
 DB 242 TEKLIHGAIFLSLSDNGTILIEPNGFTAEQDKDIMEIKVRE-GRISBTSMSTAKY 300
 QY 383 GDRKPMELDCQVDIAFPCATONEIDEHDAELLIKHCOYVEGANMPSTNEAIHKYKAG 441
 DB 301 -BGRPMVAVYEGKVDVIMPCATONEVNGTEARVYKGLVYSGAGNMPSTNEAIHKYKAG 359
 QY 442 AGITCPGKAANAGVAVGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRY--N 501
 DB 360 SKVYEGPAKSNAGVAVTSGLEMTQNRMSLNTREBVRDLERIMKDIYDSAMGSPRRY--N 419
 QY 502 V--DLAAGANIAGFTKVADAVKAGAV 526
 DB 420 KKGNYQFANVAGFTKVADSMIDQCV 446
 RESULT 5
 Q7R3N7 PRELIMINARY; PRT; 449 AA.
 AC Q7R3N7; (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE GLP 39 39379 38030.
 OS Giardia lamblia ATCC 50803.
 CC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxId=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RT Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC	preliminary data.					
DR	EMBL; AACB81000014;	EAA41919.1;	--			
DR	HSSP; P24295;	IADP.				
DR	GO; GO:0016491;	F:oxidoreductase activity; IEA.				
DR	GO; GO:0006520;	P:amino acid metabolism; IEA.				
DR	InterPro; IPR006095;	GLFV_dehydrog_N.				
DR	InterPro; IPR006096;	GLFV_dehydrog_C.				
DR	InterPro; IPR006097;	GLFV_dehydrog_N.				
DR	pfam; PF00208;	GLFV_dehydrog_1.				
DR	pfam; PF02812;	GLFV_dehydrog_N; 1.				
DR	PRINTS; PR00082;	GLFPHDRGNASE.				
DR	PROSITE; PS00074;	GLFV_DEHYDROENASE; 1.				
SQ	SEQUENCE	449 AA;	49734 MW;	239783kDa	FFBBBCAE2 CRC64;	
Query Match	48.8%;	Score 1357.5;	DB 2;	Length 449;		
Best Local Similarity	58.4%;	Pred. No. 2.9e-82;				
Matches	261;	Conservative	66;	Mismatches	111;	Indels 9; Gaps 5
QY	86 VRQLTTEFMKDPDEQEFMQANREVAVSIQPPEFKRPLPIFFKQIVPERITTRVSUL	145				
Dd	6 IEELLAVIKQRGHMTFRQAEEVVDLSKVLFEERPKYIPLEFRLLBERVIIFRVPMW	65				
QY	146 DDAGNLQVNRRGRVVOYSASIGPYKGLRHPSPVNISIMKFLAFEOIFKSLFTLTPMGSK	205				
Dd	66 DDAGLNINNRGRVYNNSALGPYKGLRHPSPVNISILKFLGFEOILKNSLTLLPMGSK	125				
QY	206 GGSDPDPKGSDAEVMRFQSFMTELORHISYVDVPADIGVGAREIGYLFQYKRITK	265				
Dd	126 GGSDPDPKGSNDENVRFQSFMTELORHVADTDVPADIDVGAREIIGYLYQYKRLRN	185				
QY	266 NYTVGLTPRGQGVGGSEIRPEATYGAVLFVENYLKDKESELKGRCCLVSGAGNAYOYA	325				
Dd	186 EFTGYLTGVNVWGSGSFIRPEATYGAVYLEMCKDNNTVTIRGNVILLISGGNAQAFC	245				
QY	326 EELLEKGAIVLSLSOSGVYVEPNFGTFEQLQAVODMKKNNSARISEKYS--DTAVVV	382				
Dd	246 ETLIDLGAKVLTFSNSNGTIYDKDFNEKLHLMTLRNKR-GRVSEFDKDYPSVAYYE	304				
QY	383 GDRRKWE-LDCQVDIAPPCATONEIDEHDAILIKHGQQYVEGANMPSTEIAIHKNK	441				
Dd	305 G-KKPWFCEQGVDCIMPCTAQNEVSGDDATRLVGLGKFAVEGANMPSTAEVAHVHA	362				
QY	442 AGIYCPCGANNAVANSGLMTONRMSLNMTRREVLDKERIMKDIYDSAMGSRRTN	501				
Dd	363 KGVMTGPAKASNAGCVSVSGLEMSONSVRLQTWTAEBVDKLRIGIMGIFVACRDPAKKYG	422				
QY	502 --VDLAAGNIINGFTKVADVAVAQGV	526				
Dd	423 HPKNTQMGNANGFLKLVADSMIEQCV	449				
RESULT 6						
DHE4_GIALA						
AC	_DHE4_GIALA	STANDARD;	PRT;	449 AA.		
AC	P28724;	O21961;				
DT	01-DEC-1992	(Rel. 24,	Created)			
DT	01-DEC-1992	(Rel. 24,	Last sequence update)			
DT	29-MAR-2004	(Rel. 43,	Last annotation update)			
DE	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	(NADP-GDH) (NADP-				
OS	dependent glutamate dehydrogenase).					
OC	Giardia lamblia (Giardia intestinalis).					
OX	Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.					
OX	NCBI_TaxID=5741;	[1]				
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92218410;	PubMed=155991;				
RA	Yee J., Dennis P.P.;					
RT	"Isolation and characterization of a NADP-dependent glutamate					
RL	dehydrogenase gene from the primitive eucaryote Giardia lamblia.";					
RN	J. Biol. Chem. 267:7539-7544 (1992).	[2]				
RP	SEQUENCE OF 59-261 FROM N.A.					
RX	MEDLINE=96155200;	PubMed=8587793;				

```

RA  Montis P.T., Mayrhofer G., Andrews R.H., Homan W.L., Limper L.,
RA  By P.L.;
RA  "Molecular genetic analysis of Giardia intestinalis isolates at the
RT  glutamate dehydrogenase locus.";
RL  Parasitology 112:1-12(1996).
CC  -I- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate
CC  + NH(3) + NADPH.
CC  -I- SUBUNIT: Homohexamer (By similarity).
CC  -I- SIMILARITY: Belongs to the Glu/Leu/Phe/Val dehydrogenases family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation at
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (see http://www.isb.ch/announce/
CC  or send an email to license@isb-ebi.ch).
CC  -----
DR  EMBL; M84604; AAA29155.1; -.
DR  EMBL; U47632; AB054400.1; -.
DR  PIR; A42489; A42489.
DR  HSSP; P24295; 1AUP.
DR  InterPro; IPR006095; GLFV_dehydrog.
DR  InterPro; IPR006096; GLFV_dehydrog_C.
DR  InterPro; IPR006097; GLFV_dehydrog_N.
DR  Pfam; PF00208; GLFV_dehydrog; 1.
DR  Pfam; PF02812; GLFV_dehydrog_N; 1.
DR  PRINTS; PR00082; GLFDHRCGNASE.
DR  PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
DR  NADP; Oxidoreductase.
FT  ACT_SITE 125..125 By similarity.
FT  CONFLICT 249..249 I -> L (in Ref. 2).
SQ  SEQUENCE 449 AA; 49766 MW; 5497B35209B549F6 CRC64;
Query Match 48.7%; Score 1324.5; DB 1; Length 449;
Best Local Similarity 58.2%; Pred. No. 4,7e-82;
Matches 260; Conservative 67; Mismatches 111; Indels 9; Gaps 5
QY 86 VRQLLTLEIFMKDPEQGEFMAQVREVAVSLQPFVEKRPPELLPIKQIVPERVITFRVSWL 145
DB 6 IEELIAVIAKQDGHMTEPRQAVEEVDSLSKVI FEREPKYIDIFERMLPERVILI PRVPMW 65
QY 146 DDAGNLQVNRGFRVQYSSAIGPYKGLRFHNSVNLSTIKFLAFEDIFKNSLITLPMGGK 205
DB 66 DDAGINNRGFRVQYSSALGPYKGLRFHPSVNLSTIKFLGFEDILKNSLITLPMGGK 125
QY 206 GSDPRDPKGSDAEVMRFQSGFMTELQHSIVYDQVPAGDDIGVAREIGYFGQYKRTK 265
DB 126 GSDPDFPKGSDNEVMRFQSGFMTELQHVADTDVPAGDDIGVAREIGYLYGYKRLRN 185
QY 266 NYTGVLPFGQGEYGSSEIRPEATGYAVLFEVNTLKDKGSLSKGRCLVSGAGNVAQYCA 325
DB 186 EFTGLTGKYNKMGGSFIRPEATGYGAVYFLEBMCKDNNTVIRGNVNLSSGNAVAQAC 245
QY 326 ELLLEKGAIVLSDSQGYVTEPENGFTREQLQAVODMKKNNASRISEYKS---DIATYV 382
DB 246 EKLTLQIGKAVLTFPSDSNGTIVDKGFNEEKLAAHMLYLNKEXR-GVSESEFKQYPSVAYYE 304
QY 383 GDRRKPEE-LDCCQVDAIFPCATONEIDHDDELIIKHGCGVVGESANNPSTNEAITHKYNK 441
DB 305 G--KKPECFEGQDMCIWPCATQNEVSGDDTRLVGLGLKFAVAGANPSTAEAVHYHA 362
QY 442 AGIYCPKANAGVAVSGLEMTQNRKSLMTTREVVDKLERIMKDIYDSAMGSPRRYN 501
DB 363 KGWVYGPAAKNAGVAVSGLEMSGNSVRLQMTAEVDQKLRGIMRGIFVACRPDAKKYK 422
QY 502 --VDLAAGANIAGFTKVADAVAKQAGV 526
DB 423 HPKYNQMGANIAGFLKADVSMIEGCV 449

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ID 09HVJ7 PRELIMINARY; PRT; 445 AA.
AC 09HVJ7;
DT 01-MAR-2001 (TReMBLrel. 15, Created)
DT 01-MAR-2001 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedLocusNames=PA4588;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stever C.K., Phan X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Britkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Gardner R.L., Goltzy L., Tolentino E., Westbrook-Madman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Slater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004872; AAC07976.1; -
DR PIR; H81072; H81072.
DR HSSP; P24295; IAUP.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHGRNASSE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
DR Complete proteome.
SQ SEQUENCE 445 AA; 48856 MW; 643EB12BC64F3418 CRC64;
Query Match 48.1%; Score 1309; DB 2; Length 445;
Best Local Similarity 59.2%; Pred. No. 5.3e-81;
Matches 263; Conservative 55; Mismatches 120; Indels 6; Gaps 4;
QY 86 VROLTEIFMKDPEQOEPMQAVREVAVSLQVFEKREPLL--TFKQVPERVITTPVVS 143
DB 5 VDAFLERKRKRDPOPEFHQAVEEVLKSLWPLLEANPHYLAGLIERVEBERALLFFRP 64
QY 144 WLDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTLLPMG 203
DB 65 WVDQGRVVRVVRGRVQVSSAIGPYKGLRPHPSVNLGVLKFLAFEOYFKNSLTLLPMG 124
QY 204 GKGSGDFDPKGSDAEVMRFQSGFMTELQRHISYQDVADGIVGAREIGYFGQYKR 263
DB 125 GKGSGDFDPKGSDAEVMRFQSGFMSELRYHVGADLDVPADIGVAREIGYFGQYKR 184
QY 264 TKNYTGVLTTPKGOYSGSEIRPEATGYAVLFENVLTKDGSLSKGRCLVSGAGNVAQ 323
DB 185 SNOQTSVLTGKGLSYGSLIRPEATGFCVYFAQEMLKDRGRFDGQVVAISGSGNVAQ 244
QY 324 CAELLLEKGAIVLSLSDSGYVEPNEGFTREOLAQVDMKKKNSARISSEKSDTAAYV 383
DB 245 AARKVMEMGKIVLSLSDSGYVEPNEGFTREOLAQVDMKKKNSARISSEKSDTAAYV 303
QY 384 DRRKRWELDCQVDIAFPQATQNEIDEHDAELLIKRGCQYVVGAMPSSTNEAIHKYNK 443
DB 304 EGRBPWGLAC--DIALPCATQNEIDAEARLLANGCVCVAEGANMPSSTLBAVDLFLEAG 361
QY 444 IYRPGKAAAGCAVAGSLENTQNRMSLNTWRREVRDLERIMDIYSA-MGSRKRVN 502
DB 362 ILVAPGKASNGAGVAVSGLEMSQNAMRLRMSGEVDTLGIMQSIHHAACLLYGEQGRV 421
QY 503 DLAAGANIAGFTKVAQVAGAV 526

DB 422 NYVGANIAGFVKVADAMLAQGV 445
RESULT 8
ID 09YV71 PRELIMINARY; PRT; 444 AA.
AC 09YV71;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase, NADP-specific.
GN OrderedLocusNames=NM1710;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
NCBI_TaxID=491;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Clecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark E.B., Cotton M.D., Uitterlinden T.R., Khouri H.M.,
RA Qin H., Vamathavan U.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL; AE002521; AAF42057.1; -
DR PIR; H81050; H81050.
DR HSSP; P24295; IAUP.
DR TIGR; NM1710; -
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHGRNASSE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
DR Complete proteome.
SQ SEQUENCE 444 AA; 48490 MW; 8B2CFCA89EF7DAF CRC64;
Query Match 47.8%; Score 1300.5; DB 2; Length 444;
Best Local Similarity 57.4%; Pred. No. 2e-80;
Matches 257; Conservative 72; Mismatches 104; Indels 15; Gaps 6;
QY 85 DVROLTEIFMKDPEQOEPMQAVREVAVSLQVFEKREPLL--PIFKQVPERVITTPVVS 142
DB 3 DIALTFANLQKRNQNPQFQAVEVMSLDPLAKNPXTQGLRIYVEREVAWFRV 62
QY 143 SWDDAGNLQVNRGRFRVQYSSAIGPYKGLRPHPSVNLSTMKFLAFEOIFKNSLTLLPMG 202
DB 63 TWQDDKQVQVNRGRVQVSSAIGPYKGLRPHPTVDLGVLFKFLAFQVFNALTTLLPMG 122
QY 203 GKGSGDFDPKGSDAEVMRFQSGFMTELQRHISYQDVADGIVGAREIGYFGQYKR 262
DB 123 GKGSGDFDPKGSDAEVMRFQSGFMTELRYHVGADLDVPADIGVAREIGYFGQYKR 182
QY 263 IYKNTGVLTTPKGOYSGSEIRPEATGYAVLFENVLTKDGSLSKGRCLVSGAGNVAQ 322
DB 183 IRNEFSVLTGKGLSEMGSLIRPEATGYCVYFAQAMLQYRNSFEKRVILISSGNVAQ 242
QY 323 YCAELLLEKGAIVLSLSDSGYVEPNEGFTREOLAQVDMKKKNSARISSEKSDTAAY 381
DB 243 YAEKAIQOLAKVLTIVDSNGFVLFPDSGMTQALALILKEVRR--RVATYAKQEGLO 301
QY 382 VGDRKRWELDCQVDIAFPQATQNEIDEHDAELLIKRGCQYVVGAMPSSTNEAIHKYNK 441


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Db 302 YFEKQKPMGV--AAEIALPCATQNEIDDEBAKTLILANGCYVAGGAMPSTLGAVEQFIK 359
Qy 442 AGIIFYCGKANGAGVAVSGLEMTQNRMSLMTREEVYDRLERIMKDIYSAGMPSPRY- 500
Db 360 AGIIFYAPGKASNGGAVATSGLEMSQNAIRLSMTREEVDORLFGIMQSIHESCL---KYG 415
Qy 501 ----NVDLAAGANIAGFTKVAADAVKAQ 524
Db 416 KVGDVTVMYVNGANIAGFVKVADAMLAQ 443

RESULT 9
ID 09JUT56 PRELIMINARY; PRT; 444 AA.
AC 09JUT56;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdhA; OrderedlocusNames=NMA1964;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
RA Jajuel K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RL Nature 404:502-506 (2000).
EMBL AL162757; CAB85184.1; -.
DR PIR; B81825; B81825.
DR HSP; P24295; IAU.
DR GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006097; GLFV_dehydrog_C.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHNGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 444 AA; 48462 MW; DEFLA7B8DDEF424 CRC64;

Query Match 47.6%; Score 1294.5; DB 2; Length 444;
Best Local Similarity 57.1%; Pred. No. 5.1e-80;
Matches 256; Conservative 72; Mismatches 105; Indels 15; Gaps 6;

Qy 85 DVROLLEIFMKDPEQEFMOAVREAVSLQVFEKRELLP--IFKQIYPERVITFRV 142
Db 3 DLNLTFLANLKQKRNQOEFEHQAVEEVLDPFLAKPKYQOGLLEIVPEREVRVFRV 62
Qy 143 SWLDAGNLQVNRGRVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 202
Db 63 TWQDDKGVQVNRGRVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 122
Qy 203 GKGSGSDFDPKSKDAEYVRCQSFMTLEOHISVYDVPAGDIGVAREIGYLFQGYKR 262
Db 123 GKGSGSDPDPKSKDAEYVRCQAFMTLELRYHIGADTVPAGDIGVAREIGYLFQGYKR 182
Qy 263 ITKRYITGVLTQKQGYGSGSEIRPEATGYGAVLFEVBNVLKDGESLKGKRCVSGAGNVQ 322
Db 183 IRNFFSSVLTGKGLEWGSILIRPEATGYGCVFAQAMLTQTNDSFEGKRVLISGSGNVQ 242
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Qy 323 YCAELLEKGAIVLSISDSQGYVER-NGFTREQLQAVQDMKKNSARISEXKSDTAVY 361
Db 243 YAAEKAIQLGAKVLTYSDSNGFVLPDSGMSQAQALALILKEVRE-RVATYAKEQGLQ 301
Qy 382 VGDGRKRWELDCQVDIAFPATQNEIDDEBAKTLILANGCYVAGGAMPSTLGAVEQFIK 441
Db 302 YFEKQKPMGV--AAEIALPCATQNEIDDEBAKTLILANGCYVAGGAMPSTLGAVEQFIK 359
Qy 442 AGIIFYCGKANGAGVAVSGLEMTQNRMSLMTREEVYDRLERIMKDIYSAGMPSPRY- 500
Db 360 AGIIFYAPGKASNGGAVATSGLEMSQNAIRLSMTREEVDORLFGIMQSIHESCL---KYG 415
Qy 501 ----NVDLAAGANIAGFTKVAADAVKAQ 524
Db 416 KVGDVTVMYVNGANIAGFVKVADAMLAQ 443

RESULT 10
ID 088Q23 PRELIMINARY; PRT; 449 AA.
AC 088Q23;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Glutamate dehydrogenase.
GN Name=gdhA; OrderedlocusNames=PP0675;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., Desoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzaple E.K., Scanlan D., Tran K.,
RA Moazzar A., Ulteback T.R., Rizzo M., Lee K., Koback D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohnes J., Straetz M., Helm S.,
RA Kewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tremmler B.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative analysis of the
metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
EMBL AE016776; AAN6300.1; -.
DR HSP; P24295; IAU.
DR TIGR; PP0675; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006095; GLFV_dehydrog.
DR InterPro; IPR006096; GLFV_dehydrog_C.
DR InterPro; IPR006097; GLFV_dehydrog_N.
DR Pfam; PF00208; GLFV_dehydrog_1.
DR Pfam; PF02812; GLFV_dehydrog_N; 1.
DR PRINTS; PR00082; GLFDHNGNASE.
DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 48871 MW; EPI733B6ABC89627 CRC64;

Query Match 47.3%; Score 1287.5; DB 2; Length 449;
Best Local Similarity 58.2%; Pred. No. 1.6e-79;
Matches 259; Conservative 55; Mismatches 124; Indels 7; Gaps 4;

Qy 86 VRQLEIFMKDPEQEFMOAVREAVSLQVFEKRELLP--IFKQIYPERVITFRV 143
Db 8 VDFVFLAKQKRDQEPHQAVEEVLRTLPFLANPHYVQSGILREWVPERAVLFRVS 67
Qy 144 SWLDAGNLQVNRGRVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 203
Db 68 WDDQGVQVNRGRVYSSAIGPYKGLRPHPSVNLISIKFLAFEOIFPKSLITLTPMG 127
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Oy		204	GKGGSDPFPKGSDEBNWRFCSFMTLEORH1SYVDVAGD1GVGARE1GYLFGYKR1	263
Db		128	GKGGSDPFPKGSDBNWFRCFAFSELSLRH1GADCDVPAGDI1GVARE1GEFFGYKRL	187
Oy		264	TKNYYGVLTLPKOQVSGSREPEATGCVGLVFENVTLAKPGESLKAKRCLVSGAGVAOY	323
Db		188	ANQFISVLTKMKMTGSGSLIRREATIYGCVFAEEMLKRPQDRIDRRARVASSSGVAOY	247
Oy		324	CABLLEKGAIYALISDSOGCIYIEPNGFTRBQLQAVDMKKNNNSARISEYSKDIAVYVG	383
Db		248	AARKVMDDGGKVIYSLSDSEGLTYAENGLTDAQWDALMELKNVR-GRISBLAQCFGLBER	306
Oy		384	DRRKWEILDCQVDIFPCATONEIDEHDABELLIKHGCQYVEEGANMPSTNEATHKYNKA	443
Db		307	KQQTWSLPC--DIALPCATONELGAEADRKLTRLNRCCICVABGANPFLLBAVDITLDG	364
Oy		444	IIPCCKAAMAGVAVSGLEMONTMSLNWTREBEVDKLERIMKDIYDSAM-GPSRRYN	501
Db		365	ILYARGKSNAGCAVAVSGLEMSONMRRLMTAGEVDSXLHNINQS1HHACVHYGEADGR	424
Oy		502	VDLAAGANIAGFTKXVADAIVKAGAV	526
Db		425	INYVKANIIAGFVKVADAMLAAQGV	449
 RESULT 11 O96940				
ID	O96940	PRELIMINARY;	PRT;	470 AA.
AC	O96940;			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Glutamate dehydrogenase (NADP+)	(EC 1.4.1.4).		
GN	Name=GLDH; Synonyms=GDH;			
OS	Plasmodium falciparum.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.			
OX	NCB1_TaxId=5833;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
FX	MEDLINE=99089647; PubMed=9874251;			
RA	Wagner J.T., Luedemann H., Faerber P.M., Lottspeich F.,			
RA	Krauth-Stiegel R.L.;			
RT	"Glutamate dehydrogenase, the marker protein of Plasmodium falciparum.			
RT	Cloning, expression and characterization of the malarial enzyme.";			
RL	Eur. J. Biochem. 258:813-819(1998).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	Li L.H., Li M., Wu Y.S., Wang P.;			
RA	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; Y12927; CAA73390.1; -.			
DR	EMBL; AY040586; AAK77969.1; -.			
DR	HSSP; P24295; IADP.			
DR	GO; GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.			
DR	GO; GO:0016491; F:oxygen reductase activity; IEA.			
DR	GO; GO:0006520; P:amino acid metabolism; IEA.			
DR	InterPro: IPR006095; GLFV_dehydrtog_C			
DR	InterPro: IPR006096; GLFV_dehydrtog_C			
DR	InterPro: IPR006097; GLFV_dehydrtog_N			
DR	pfam; PF0208; GLFV_dehydrtog_1.			
DR	pfam; PF02812; GLFV_dehydrtog_N_1.			
DR	PRINTS; PR00082; GLFDHGRNASB.			
DR	PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.			
KW	Oxidoreductase.			
SQ	SEQUENCE 470 AA; 52546 MW; 50A37C348C387A CRC64;			
 Query Match 47.3%; Score 1286.5; DB 2; Length 470; Best Local Similarity 55.2%; Pred. No. 1.9e-79; Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7				
Oy	48 ISAMATTGDFFALQCAVAVQMATAKTGELVNH1KNPDVQRQLTE1FMKPDEQDFMQAF	107		
Db	1 MSALKDKTGFRFVLD-----NASYESLV----DQENNMYVERVWKCDPNQVETFLQAF	50		

QY	108	REVALSVLOPVEPKKPELLPIFKOIVBEERATVFEVSMDDDGNQVNRGPFVQSSAIGP	167
Db	51	HEILYSLKPFLMEBPXTLPITETISEBRALQFVCMDDNGVQRKRCFRVQVNSALGP	110
QY	168	YKGLRFRPFSVNSIMKFLAFBEQIFKNSLTLLPMGSGKSGSDPDKGSDAEVNRFCQSF	227
Db	111	YKGLRFRPFSVNSIMKFLAFBEQIFKNSLTLLPMGSGKSGSDPDKGSDAEVNRFCQSF	170
QY	228	MTELORHISTYQVDPADIDIGVGAAREIGTLGQYQKRIKNTKNTGULTPKQEGEGSEIRPEA	287
Db	171	MNELYRRIHGPCTDPADIDIGVGAAREIGTLGQYQKRIKNTKNTGULTPKQEGEGSEIRPEA	230
QY	288	TGYCAVLFVEVAVLKDKGESLKGKRCCLVSGAGNVQYCAELLEKGAIVLSLSDQGYE	347
Db	231	TGYCAVLFVEVAVLKDKGESLKGKRCCLVSGAGNVQYCAELLEKGAIVLSLSDQGYE	290
QY	348	PNGFTREBQLOAVODMKKKNNSARISEY--KSDTAVVYGDRRRKPEWELDCQVDAIFPCATON	405
Db	291	PNGFTREBQLOAVODMKKKNNSARISEY--KSDTAVVYGDRRRKPEWELDCQVDAIFPCATON	346
QY	406	EIDEDHDELKIKHCCQVVGAGNANPSTNEAHKKNKAGITTCPEKANAGSVAVSGLEMT	465
Db	347	EINEDAKLQIKXNCILLVBEGANNPSTVDALNLPKSNNTIYCPSKANAGSVAVSGLEMT	406
QY	466	ONRMSLWMTREBVVDKLERIKIDYDSBAMGFSRRY--NVDLAGANLAGEFTKADAVKA	522
Db	407	ONPFSWHTRETVDBKLEIKEMRNFIACSEBALKTYTKNKYDLOGANLAGEFTKADAVKA	466
QY	523	QG 524	
Db	467	QG 468	
RESULT 12			
Q8IL1T0		PRELIMINARY; PRT; 470 AA.	
AC	Q8IL1T0		
DT	01-MAR-2003 (TREMblurel. 23, Created)		
DT	01-MAR-2003 (TREMblurel. 23, Last sequence update)		
DT	01-OCT-2003 (TREMblurel. 25, Last annotation update)		
DE	NADP-specific glutamate dehydrogenase.		
GN	ORFNames=PF14_0164;		
OS	Plasmodium falciparum (isolate 3D7).		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.		
OX	NCBI_TaxID=36329;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;		
RA	Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,		
RA	Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,		
RA	Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,		
RA	Chan M.S., Nene V., Shallow S.J., Sub B., Peterson J., Angiolini S.,		
RA	Pertea W., Allen J., Selengut J., Haft D., Mather M.W., Vaizy A.B.,		
RA	Martin D.M., Fairlair A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,		
RA	McCracken G.I., Cummings L.M., Subramanian G.M., Mungall C.,		
RA	Venter J.C., Caracci D.J., Hoffman S.L., Newbold C., Davis R.W.,		
RA	Fraser C.M., Barrell B.;		
RT	"Genome sequence of the human malaria parasite Plasmodium		
RT	falciparum."		
RL	Nature 419:498-511(2002).		
DR	EMBL; AE014818; AAN36776.1; -.		
DR	HSSP; P24295; IAU.		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0006520; P:amino acid metabolism; IEA.		
DR	InterPro; IPR006095; GLFV_dehydrog.		
DR	InterPro; IPR006096; GLFV_dehydrog_C.		
DR	InterPro; IPR006097; GLFV_dehydrog_N.		
DR	Pfam; PF00208; GLFV_dehydrog; 1.		
DR	Pfam; PF02812; GLFV_dehydrog; 1.		
DR	PRINTS; PR00082; GLEFHDRGNASE.		
DR	PROSITE; PS00074; GLFV_DEHYDROGENASE; 1		
SO	SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC64;		

Query Match 47.3%; Score 1286.5; DB 2; Length 470;
Best Local Similarity 55.2%; Pred. No. 1.9e-79;
Matches 266; Conservative 64; Mismatches 133; Indels 19; Gaps 7;
QY 48 ISMDATGCTGTAATGKATAGTGGVHGKAPDVRQLTETMKDPEQOEPMQAV 107
DB 1 MSAAKDTGTRVVLDK-----NANSNYSLV---DDEMNVYERVKLTPNQVEFGQAF 50
QY 108 REVAVSLQPVPEKAPPELLPFKQIVPEPVITFRVSWLMDAGNLQVNRGFRVQSSAIGP 167
DB 51 HEIYISLKLPLFMEEPKLPILITETSEPRALQFVWCHLDNGVRKAKRCRVQYNSALGP 110
QY 168 YKGLRFPSPVNSLIMKFLAEQIFKNSLTTLPMGGKGGSDPDKKSDAEVNRFCQSF 227
DB 111 YKGLRFPSPVNSLIMKFLAEQIFKNSLTTLPMGGKGGSDPDKKSDAEVNRFCQAF 170
QY 228 MTELQRIISYQVDPADIDIGVGAETGYLFGQYRITKNNTGVLTTPKQGEYGSSEIRPEA 287
DB 171 MNELYRHIGPCTDVPADIDIGVGAETGYLFGQYRITKNNTGVLTTPKQGEYGSSEIRPEA 230
QY 288 TGYGAVLFVENVLKDKGESLKKRCLVSGAGNVAQCAELLLEKGAIVLSLSDSQGYVE 347
DB 231 TGYGLVFLVEVLSLIMPEVKQDAVVGSGSNVALYCVQKLLHNVKVLTLSDSGYVE 290
QY 348 PNGFTREQLQAVQDMKKNSARISEY--KSDTAVVYGDRRKPEWELDCQVDIAFPCCATON 405
DB 291 PNGFTHENLEFLDLKEB-KKGRITKEYLHNSSTAKYF-PNEKPMGVPC--TLAPPCATON 346
QY 406 EIDEDHALLIKGCQYVVBGANNPSTNEAIHKYKNGKGIYCPKKAANAGVAVSGLEMT 465
DB 347 EIMEDAKLLQKNCILVGBGANNPSTVDIINLFKSNIIYCPKKAANAGVAVSGLEMS 406
QY 466 QNRSLMTREEVADKLERIKQDLYDSAMGSPRY---NVDLAAGNIAGFTKYADAVKA 522
DB 407 QNFPFSMTRETVDEKLEIKEMRIFACSENALKYTKQKTDLOGANIAGFLKVAESYIE 466
QY 523 QG 524
DB 467 QG 468

RESULT 13
Q923C4 PRELIMINARY; PRT; 445 AA.
AC Q923C4; 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 03-JUL-2004 (Tremblrel. 27, Last annotation update)
DE NADP-glutamate dehydrogenase (EC 1.4.1.4).
GN Name=gdh;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAOI;
RA Ansari F.;
RA Thesis (1994), University of London, London U.K.
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=PAOI;
RA Brown P.R.;
RL Theis (1994), University of London, London U.K.
EMBL: Y18494; CAA77192.1; -;
DR EMBL: Y15166; CAA75437.1; -;
DR HSSP: P24295; IAUJ.
DR GO: GO:0004354; F:glutamate dehydrogenase (NADP+) activity; IEA.

DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR006095; GLFV_dehydrog.
DR InterPro: IPR006095; GLFV_dehydrog_C.
DR InterPro: IPR006097; GLFV_dehydrog_N.
DR Pfam: Pf00208; GLFV_dehydrog_1.
DR Pfam: Pf02812; GLFV_dehydrog_N; 1.
DR PRINTS: PR00082; GLFDHGRNAS.
DR PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.
DR Oxidoreductase.
KW SEQUENCE 445 AA; 48532 MW; B0DDDEBE03A06D8A CRC64;
SQ
Query Match 47.2%; Score 1285; DB 2; Length 445;
Best Local Similarity 58.4%; Pred. No. 2.3e-79;
Matches 261; Conservative 56; Mismatches 118; Indels 12; Gaps 5;
QY 86 VRQLLEIFPKDPEQOEPMQAVNEVAVSLQPVPEKAPPELL--IFKQIVPEPVITFRVS 143
DB 5 VDAFLERLKRDRDQDEFFHQAVEVLRSLMPLEANPHYLEAGIIRIVPEPALIFRVP 64
QY 144 WLDDAGNLQVNRGFRVQSSAIGPYKGLRFPSPVNSLIMKFLAEQIFKNSLTTLPMGG 203
DB 65 WDDQGRVNRGRVQSSAIGPYKGLRFPSPVNSLIMKFLAEQIFKNSLTTLPMGG 124
QY 204 GKGSDFDPKKSDAEVMRFGQSFMTLQRIISYQVDPADIDIGVGAETGYLFGQYKRI 263
DB 125 GKGSDFDPKKSDAEVMRFGQSFMTLQRIISYQVDPADIDIGVGAETGYLFGQYKRI 184
QY 264 TKNYTVLTPKQGEYGSSEIRPEATGYAVLFVENVLKDKGESLKKRCLVSGAGVAVQY 323
DB 185 SNFTSVLTGKGSYGSGLTRPEATFGCYFAQEWLKKRGKGFDCQRVASISGQVAVQY 244
QY 324 CABLLEKGAIVLSLSDSQGYVEPNFTREQLQAVQDMKKNSARISEYKSDT--AV 380
DB 245 AAKRVMEGSKVLSLSBSGTLAEAGLSDBQWEYLMELK---NAPAGHPRGVEQFSL 300
QY 381 YVGDRRKPEWELDCQVDIAFPCCATONEIDEDHALLIKGCQYVVBGANNPSTNEAIHKYN 440
DB 301 QPLEGVPPWGLAC--DIALPCATONELDAEDARLLANGVCVAEGANNPSTLEAVDLFL 358
QY 441 KAGIYCPKKAANAGVAVSGLEMTNRMSLNTREBVRDKLERIKQDLYDS-MGPSRR 499
DB 359 EAGILYAPGRASNAGVAVSGLEMSQANMLRWSBGEVDTKLGIQSIHHACLGLGEEQ 418
QY 500 YNVDLAAGNIAGFTKYADAVKAQAV 526
DB 419 GRVNYVKGANIAGFKVADMLAQGV 445

RESULT 14
Q7YZU7 PRELIMINARY; PRT; 437 AA.
AC Q7YZU7; 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Glutamate dehydrogenase (Fragment).
GN Name=gdh.
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalia; Trichomonada; Trichomonadida;
OC Trichomonadidae; Trichomonadinae; Trichomonas.
OX NCBI_TaxID=5722;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12820901; DOI=10.1186/1471-2148-3-14;
RA Andersson U.O., Roger A.J.;
RT "Evolution of glutamate dehydrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes."
RL BMC Evol. Biol. 3:14-14(2003).
EMBL: AF533886; AAP83853.1; -;
DR HSSP: P24295; IAUJ.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.

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